Run on:

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August 3, 2004, 17:17:11; Search time 685.5 Seconds (without alignments) 1770.394 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tptio	SK6064 or minutes	9175 Dengue v	9176 Dengue	496 Se	2036 Dengue vi	2040 Dengue	2044 Dengue	2048 Dengue	2052 Dengue	2060 Dengue	2064 Dengue	12068 Den	2012 Dengue	2080 Dengue	2084 Dengue	2088 Dengue	2092 Dengue	2104 Denque	2108 Dengue	2112 Dengue	2120 Dengue	2124 Dengue	2128 Dengue	2132 Dengue	2136 Dengue	2148 Dengue	2152 Dengue	2156 Dengue	2160 Dengue	2164 Dengue	2172 Dengue	2176 Dengue	2180 Dengue	2164 Dengue	2192 Dengue	2196 Dengue	2200 Dengue			linear VRL 0	virus DEN4, H241-P, Genomic,				s. no DNA stage; Flaviviridae;		Lai, C.J.	virus neurovirulence for mice
SUMMARIES	966064	AF469175	AF469176	AR232496	AVISONAGE	AY152040S1	AY152044S1	AY152048S1	AY1520551 AY15205681	AY152060S1	AY152064S1	AY15206881	AT1520/251	AY152080S1	AY152084S1	AY15208831	AY15209251	AY152104S1	AY152108S1	AY15211281	AT15211651 AY15212051	AY152124S1	AY152128S1	AY152132S1	AY152136S1	AY152148S1	AY15215281	AY152156S1	AY152160S1	A115216451 AV15216851	AY15217281	AY152176S1	AY152180S1	A113216431	AY15219251	AY15219651	AY152200S1	AL TGNMENTS		2319 bp DNA	[dengue type				strand viruse	rus group.	,V., Rosen,L. and	dengue type 4
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Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
AF469176
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Dengue virus type 2
Viruses; sexNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
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Pred. No. 0.89;
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/note="contains structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ren, R.W., Fang, M.Y., Tian, X.D.,
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Unpublished
2 (bases 1 to 2325)
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Best Local Similarity 89.3%;
Matches 25; Conservative
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MVLAFITFLRVLSIPPTAGILKRWGQLKKNKAIKILTGFRKEIGRMLNILNGRKRSTM
MVLAFITFLRVLSIPPTAGILKRWGQLKKNKAIKILTGFRKEIGRMLNILNGRKRSTM
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EVKLPDYGELTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLELPWAAGADTSSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVVGRIISPTPFAENTNSVTNIELERPLÖSYIVIGVGDSALTLHWFRKGSSIGKMFES
TYRGAKRMAILGETAMDFGSVGGLLTSLGKAVHQVFGSVYTTMFGGVSMMVRILIGFL
VLMIGTNSRNTSMAMTCIAVGGITLFLGFTVQA"
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Dengue virus type 2
Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
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RMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYFGGAGAPCKVPIEIRDVNKE
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Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
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Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
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AF469175
                                                                       GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 138430] from the original journal article. This sequence comes from Fig. 1.
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89.3%; Pred. No. 0.89;
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/note="This sequence comes from Fig.
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  (11), 6567-6575 (1993)
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Matches 25; Conservative
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                                                                          REMARK
                                                                                                                                                    PEATURES
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AUTHORS
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KLEMALVAFLRFLTI PPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLNI LNFRRRSA
GWI IMLI PTVWAFHLTTRNGEPHM IVS I QEKGKS LLFKTEDGVNMCTLMAMDLGELCE
DEN IT YKCPLLRQNEPEDI DOKONSTSTAVI YGGTTTGGHRREKRSVALPHVGMGLE
TRTETWASSEGRAMAQRI ETWI LHHPGFTI MAAI LAXTIGTTHFQRALI FILLTAVA
PSMTMRCI GI SNRDFVEGVSGGSWVDI VLEHGSCVTTMAKNFPTLDFELI KTEAKQPA
                                                                                                 TLRKYCIEAKLINTTTESRCPTGGEPSLKEEQDKRFVCKHSIVDRGWGNGGGLFGKGG
VYCAMFTCKKGNMEGKIVQPSNLEYITVTPHSGSEBJAIGNDTGKHGRSIKYTPDSSV
TEAELIGYGTYTIESPRTGENSWYLLQMKGNKAMIVHGQMFLDLFLPWLPGADTGG
SNWIQKETLYTLKNPHAKKQDVVVLGSQBGAMHTALTGATEIQMSGNILLFTGHLKCR
                                                                                                                                                                               LRMDKLQLKGMSYSMCTGKFKVVKEJAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEK
YYLGKLITVNPIVTEKDSPVNIEDVPFGDCYIIGYRBGQLKLNWFKKGSSTGQMF
ETTWRGAKRWAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWTMKILIG
VIITWIGMNSRSTSLSVSLVLVGIVTLYLGVMVQA"
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Dengue virus type 2
Viruses; BSRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
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Gruenberg, A., Woo, W.S., Biedrzycka, A. and Wright, P.J.
Gruenberg, A., Woo, W.S., Biedrzycka, A. and Wright, P.J.

Partial nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue virus type 2, New Guinea C and PUO-218 strains
J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dengue nucleic acid vaccines that induce neutralizing antibodies
Patent: US 6455509-A 1 24-SEP-2002;
Location/Qualifiers
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Kochel,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
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                                                                                                                                                                                                                                                                                                   Score 25; DB 14; Length 2325;
Pred. No. 0.89;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1 from patent US 6455509.
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/wol_type="genomic RNA"
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.3%;
Matches 25; Conservative
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Guinea C.
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D00346.1 GI:221230
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DENZNGC/c
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AUTHORS
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DTITYKCPPLRQNEPEDIDCWCNSTSTWYTYCTCTTTGEHRREKRSVALVPHVGMGLE
TRTETWASSEGARKHAQRIETWILAHPGFTIMALILAYTIGTHFRORALIFILETRIAVA
PSWTWASCEGARKHAQRIETWILAHPGFTIMALILAYTIGTHFRORALIFILTRANA
PSWTWRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPA
TURKYCIEAKLTWYTTDSRCPTQGEBSLNEEQDKRFVCKHSWVDRGWGNGGGEGKGG
IVTCAMFTCKKNWKGKVVQPENLEYTIVITPHSGEBELAVGNDTGHGKEIKITPOSSI
TEAELIGYGTVTWRCSPRTGLDPREWVLLQMENKAMLVHRQWFLDLPLPWLPGADTQG
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IRMDKLQLKGMSYSMCTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEIMDLEK
RWIGKLALTVYPROMSYNNIBAEDFFGDSYIIGTUTGVESGGIGGMI
ETTWRGAKRWALLGDTAMDFGSLGGVFTSIGKALHQVFGAIYGAAFSGUSWTWKLLIG
VIITWIGMNSRSTSLSVSLVLVGVVTLYLGVNVQADSGC
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Dengue virus type 4 (DEN-4)
Dengue virus type 4 (DEN-4)
Dengue virus type 4 (DEN-6)
Dengue virus type 4 (DEN-6)
Dengue virus type 4 (DEN-6)
Elavivirus; Dengue virus group.
1 (Deses I to 2552)
Bennett, S. M., Holmes B.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="miniorkkarntpenmikrernrystvooltkresigmiloergdi
Klemalvapirpeltipptagiikrmgtikkskainvirgfrksigrminiinrrrta
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Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial
                                                                                                                                                                       /mol_type="genomic RNA"
/errain="New Guinea C"
/bxref="Lexon:11060"
/noce="20bp upstream from the C protein amino terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                             nucleotide 77
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Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
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                             le 1 in the NGC sequence corresponds to nuc
from the 5'end of the DEN-2(JAM) sequence.
Location/Qualifiers
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/codon start=1

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organism="Dengue virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363. .860
/product="prM protein"
636. .860
/product="M protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="NS1 protein"
/note="amino end"
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/product="C protein"
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AY152036.1 GI:28170806
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Best Local Similarity 89.3
Matches 25; Conservative
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Nucleotide 1
counting from
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SYGMRCVGVGNRDFVEGWILNRPGFALLAGFMAYMIGGTGIGKGGV
URTYCIEAAISNITTATRCFPQGEPTLKEDGDQYITRRDVVDRGWGNGGGLFGKGGV
VTCAKFSGSGKITGNLVQIENLETYVVVTVHNGDTHAVGNDTSNHGVTATITPRSPSV
EVKLADYGELTLDGERRAGDVYTVLGSQEGAMHSALAGATEVDSGDGKNMFAGHLKCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses, ssRNA positive-strand viruses, no DNA stage, Flaviviridae,
Flavivirus, Dengue virus group.
I (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMEKLRI KGMSYTMCSGKPS I DKEMARTQHGTTVVKVYKYEGAGAPCKVPI E I RDVNKE
KVVGRVI SSTPLABNTNSVTNI E LEPPEGDSY I V I CVGNSALJTHWFRKGSSI GKMFE
STYRGAKRMA I LGETAMDFGSVGGLFTSLGKA VHQVFGSVYTTMFGGVSMI R I LI I GP
LVLM I GTNSR NTJSKAMTCI A VGGTTLFLGFTVQADMGCVSPSGRELKCGSGI FVVDN
VHTWTEQYKPQPESPARLASA I LNAHKDGVCGI RSTTRLENVMWKQI I VBELN
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Dengue virus type 4 D4.18_1998 polyprotein precursor, gene, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (1898-289-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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/mol type="genomic RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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                                                                                                         /note="acronym: DEN-4"
                                                                                                                                                                                                          codon start=1
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AY152044.1
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Dengue virus type 4
Viruses; saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses; saRNA positive-strand viruses, no DNA stage; Flaviviridae;
I (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMEKLRIKGMSYTMCSGKFSIDKEMAETOHGTTVVKYKYEGAGAPCKVPIEIRDVNKE
KVVGRVISSTPLAENTNSVTNIELEPPFGDSYIVIGVGNSALTLHWFRKGSSIGKMFE
STYRGAKRMAILGETAWDFGSVGGLFTSLGKAVHQVFGSVYTTMFGGVSWMIRILIGF
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VHTWTEQYKIQPESPARLASAILNAHKDGVCGIRSTTRLENVMWKQITNELN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY152040S1 25-22 bp RNA linear VRL 29-SEP-2003
Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial
                                                                                                                                                                                                                                                                                                                                      'note="contains core protein, matrix protein and envelope
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Direct Submission
Submitted (18-5EP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico Location/Qualifiers
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AY152040.1 GI:28170815
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RMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAPCKVPIEIRDVNKE
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Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus, Dengue virus group.
I (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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STRGAKRMALLGETAMDFGSVGGLFSLGKANHQVFGSYTTNFGGGVSWMIRLLIGF
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VHTWTEQYKFQPESPARLASAILNAHKOGVCGIRSTTFLENVWWKQITNELN
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Dengue virus type 4 D4.14_1998 polyprotein precursor, gene, partial
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/note="contains core protein, matrix protein and envelope
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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Pred. No. 0.88;
0; Mismatches 3; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 CCCATCTTCAGAATCCCTGCTGTTGG 178
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Best Local Similarity 89.3%;
Matches 25; Conservative
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VHTWTEQYKFQPESPARLASAILNAHKDGVCGIRSTTRLENVMWKQITNELN"
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1 (bases I to 2552)

1 (bases I to 2552)

Bennett, S. N., Holmes B.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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'note="contains core protein, matrix protein and envelope
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Birect Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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Pred. No. 0.88;
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89.3%; Pred. No. v.c.
0; Mismatches
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
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/codon_start=1
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AY152052.1 GI:28170842
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HWNYKERMYTFKVPHAKRQDYTVLGSQEGAMHSALACATTEVDSGDGMIMFAGHLKCKV
RMEKLRIKGMSYTMCSGKFSIDKEMAETQHCTTVVKYKYEGAGAPCKVPIEIRDVNKE
KVOKRVISSTPLAENTNSVTNIELEPEPFGDSYIUTGVGNAALTLHWFRKGSSIGKMFE
STYRGAKRAAILGETAMPGSGYGLFTSLGKAVHQVFGSVYTMFGGVSWM RILIGF
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LVIMIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVVSNSGRELKCGSGIFVVDD
VHTWTEQYKFQPESPARLASAILNAHKDGVCGIRSTTRLENVMMKQITNELN
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Dengue virus type 4
Viruses; saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Brol. 20 (10), 1650-1658 (2003)
HWNYKERMVTFKVPHAKRODVTVLGSQEGAMHSALAGATEVDSGDGNHMFAGHLKCKV
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Dengue virus type 4 D4.17_1998 polyprotein precursor, gene, partial
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                                                                                                                                                                                 Score 25; DB 14; Length 2552;
Pred. No. 0.88;
0; Mismatches 3; Indels
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/isolate="b4.17_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
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/codon start=1
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ilarity 89.3%;
Conservative 0
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TVYTKCPLLVNTFPEDIDGWCNLTSTWWWYGTCTQGGERRRERRSVALTPHSGWED
TVYTKCPLLVNTFPEDIDGWCNLTSTWWYGTCTQGGGRRRERRSVALTPHSGWED
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LRTYCTBASISHITTATRCPTQGEPVLKEGDQQYTCRRDVURGWGNGGGGGVGV
VTCAKFSCGGGITTGANLVGIRNLEYTVWYTVHWGNPTSNHGVTATITPRRSPSV
EVYLLDDGPRSGITGHNENILLMKWKKKTWLVHKQWFLDLPLPWTAGADTSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus, Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Mol. Stoll. Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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KVVGRVISSTPLAENTNSYTNIELEPPFGDSYIVIGVGNSALTLHWFRKGSSIGKMFE
STYRGAKRMAILGETAMDFGSVGGLFTSLGKAVHQVFGSVYTTMFGGVSMMIRILIGF
LVLMIGTHSRNTSKAMTCIAVGGTTLELGFTVQADMGCVVSKGSRELKCGSGIFVVDN
VHTWTEQYKFQPESPARLASAILNAHKDGVCGIRSTTRLENVMWKQITNELN"
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Dengue virus type 4 D4.45_1998 polyprotein precursor, gene, partial
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (14-8EP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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                Score 25; DB 14; Length 2552;
Pred. No. 0.88;
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                                                                         3; Indels
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/mol type="genomic RNA"
/molace="D4.45_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
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89.3%; Pred. No. v..
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TITLE JOURNAL PUBMED

REFERENCE AUTHORS

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PEATURES

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Dengue virus type 4 (DEN-4)
Dengue virus type 4 (DEN-4)
Dengue virus type 4 (DEN-4)
Viruses, seRNA positive-strand viruses, no DNA stage, Flaviviridae,
Flavivirus; Dengue virus group.
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RMEKLRI KRMSYTMCSGKFSI DKERABETQHGTTVVKYKYEGAGAPCKYP I EI RDVNKE
KVVGRVI SSTPLAENTNSVTNI ELEPFEDSY I VIGVGNSALTLHWFRKGSSI GKMFE
STYRGAKRAA I LGETAMPEGSVGLEPFIGGAVHQVFGSVYTMFGGVSWMIR I LIGF
LVLM IGTNSRNTSMAMTCI AVGGI TLELGFTVQADMGCVVSNGGRELKGGSGI FVVDN
VHTWTEQYKFQPESPARLASAI LLAHKDGVCGIRSTTRLENVWMKQI TNELN"
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/note="contains core protein, matrix protein and envelope
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Belltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
                                                                                                                                                                                                                  Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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Pred. No. 0.88;
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/isolate="D4.13_1998"
/db_xref="taxon:11070"
/country="Puerto Rico"
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
                                              GI:28170878
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/codon_start=1
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Matches 25; Conservative
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Dengue virus type 4 D4.47_1998 polyprotein precursor, gene, partial
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1 (bases 1 to 2552)
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HMNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHMFAGHLKCKV
RMEKLRIKGMSYTMCSGKFSIDKEMAETQHGTTVVKVKYEGAGAPCKVPIEIRDVNKE
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LVLWIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVVSWSGRELKCASRIFVVDN
VHTWTEQYKFQPESPARLASAILNAHKDGVCGIRSTTRLENVMWKQITNELN"
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LOCUS AY15206851 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.13_1998 polyprotein precursor, gene, partial
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note="contains core protein, matrix protein and envelope
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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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(codon_start=1
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Viruses, seRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.

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Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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SYRGAKRMAALLGETAMDFGSVGGLFFGLGKAVHQVFGSYTTWFGGGVSWNIRLIIGF
LULMIGTNGRNTSMAALTA VGGTTLFLGFTVQADMGCVVSWGGRELKCGSGIFVVDN
VHTWTEQYKFQPESPARLASALILAHKGGVCGIRSTTRLENVWMKQITYRELN
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/note="contains core protein, matrix protein and envelope
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Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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/mol type="genomic RNA"
isoTate="D4.46 1998"
/db xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
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Query Match 89.3%; Score 25; DB 14; Length 2552; Best Local Similarity 89.3%; Pred. No. 0.88; Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps

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Search completed: August 3, 2004, 19:08:56 Job time : 686.5 secs

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ALIGNMENTS

New dengue virus-specific primers, useful for reverse transcriptase-polymerase chain reaction assays, particularly for detecting or quantitating dengue virus in a sample. PCR; primer; 88; reverse transcriptase; RT-PCR; dengue fever; DF; dengue haemorrhagic fever; virus; viral detection. /*tag= c /mod_base= i /note= "deoxy-inosine" /*tag= b /mod_base= i /note= "deoxy-inosine" /*tag= a /mod_base= i /note= "deoxy-inosine" Dengue virus detection PCR primer #1. Location/Qualifiers ABX15697 standard; DNA; 28 BP. 28-FEB-2002; 2002US-00085944. 01-MAR-2001; 2001US-0272535P 31-MAR-2003 (first entry) WPI; 2003-182625/18 US2002155435-A1 (WANG/) WANG W. Key modified_base modified_base modified_base Dengue virus 24-OCT-2002. ABX15697;

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                                                                 This invention relates to novel Dengue virus reverse transcriptase (RT) PCR primers which may be used to detect Dengue virus in a sample. Dengue virus is a member of the flavivirus family and causes diseases including dengue fever (DF) and dengue hemorrhagic fever. The invention also comprises a method for detecting and quantitating dengue virus. The dengue virus specific primers of the invention are useful in reverse transcriptase-polymerase chain reaction assays, particularly for detecting or quantitating dengue virus in a sample. The present sequence represents a dengue virus specific RT-PCR primer used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New pharmaceutical compositions containing dengue nucleic acids, useful as a vaccine, particularly for inducing a protective immune response in mammalian subjects against the dengue virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical; ds; immune response; immunogenic; envelope; membrane; PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen; mosquito; Aedes aegyptii; acute undifferentiated fever; dengue adengue haemorrhagic fever; DHF; dengue shock syndrome; DSS; immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
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                           Claim 25; Page 1; 6pp; English
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also appears on the virion surface and is required for proper processing of the envelope protein. Dengue viruses are transmitted primarily by the mosquito, Aedes aegyptii, and can lead to human illnesses ranging from acute undifferentiated fever to dengue haemorrhagic fever (DHF) and dengue shock syndrome (DSS). Secondary infections, with a different serotype, may lead to an immune enhancement phenomenon. The compositions of the invention are DNA vaccines which are injected into the animal as a particularly for inducing a protective immune response in mammalian subjects against the dengue virus infection. The sequence presented is the dengue virus type 2 (Den 2) structural gene genome segment
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                                                                                                                                                                                                                                                                                                                                          Gaps
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/product= "DEN4 strain rDEN2/4delta30 protein"
                                                                                                                                                                                                                                                                                         Score 25; DB 7; Length 2357; Pred. No. 0.29;
                                                                                                                                                                                                                                                       Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        3; Indels
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'product= "Anchored capsid protein'
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                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/*tag= k
/product= "NS4A protein"
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478. .4131
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product= "NS3 protein"
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97. .10263
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/*tag= 1
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(*tag= q
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1 Similarity 89.3%;
25; Conservative
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WPI; 2003-120809/11.
P-PSDB; AAE35313.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          New mutated flavivirus, useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 7; Length 10616;
Pred. No. 0.37;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 CCCATCTCTTCAGTATCCCTGCTGTTGG 277
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                                 /product= "NS4B protein"
7561. .10260
/*tag= n
                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES (BLAN/) BLANEY J E.
                                                                              /product= "NS5 protein"
'product= "2K protein"
                                                                                                                                                                                                                                                          whitehead SS, Murphy BR, Hanley KA
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102. .10649
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/product= "DEN4 8
102. .440
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ID AAD53911 standard; DNA; 10649
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                                                                                                                                                                                        22-MAY-2001; 2001US-0293049P
            6826. .7560
/*tag= m
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Best Local Similarity 89.3%;
Matches 25; Conservative
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P-PSDB; AAE35314.
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               mat_peptide
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The present invention relates to novel mutated flaviviruses comprising a phenotype in which the viral genome is modified by introduction of a mutation, singly or in combination, taken from mutations from recombinant virus bearing Vero adaptation mutations, putative Vero cell adaptation mutations of dengue type 4 virus (DEN4) or mutations of the invention are useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and youth characteristics of infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutated flavivirus, useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection.
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                                                                                           "Membrane precursor protein"
                     "Virion capsid protein"
                                                                                                                                                                                                                                "Envelope protein
                                                                                                                                                               "Membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 131-132; 246pp; English.
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product= "NS3 protein"
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'*tag= j
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*tag= 1
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*tag= h
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441. .938
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Matches

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RESULT 5 AAD53910/c

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The present invention relates to novel mutated flaviviruses comprising a phenotype in which the viral genome is modified by introduction of a mutation, singly or in combination, taken from mutations from recombinant virus bearing Vero adaptation mutations, putative Vero cell adaptation mutations of dengue type 4 virus (DEN4) or mutations of the invention are useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection. The present sequence is Dengue virus type 4 strain 2A DNA
                                                                                                                New mutated flavivirus, useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;
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97. .1026
/*tag= a/product= "DEN-2/3-VP1 fugion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 CCCATCTTCAGAATCCCTGCTGTTGG 279
                                                                                                                                                                           Disclosure; Page 123-126; 246pp; English.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(BLAN/) BLANEY J E.
                                           Hanley
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(first entry)
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les 25; Conservative
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Dengue virus; type III.
Chimeric.
                                           Whitehead SS, Murphy
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P-PSDB; AAE07984.
                                                                        WPI; 2003-120809/11
                                                                                      P-PSDB; AAE35312
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01-NOV-2001
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0; Mismatches
                                                        306 cccarcrcrcagaarcccrccrcrrgg 279
                            1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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/product= "NS2A protein"
1134. .4523
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5759. .6827
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product= "NS2B protein"
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7563. .10262
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'product= "NS1 protein"
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                                                                                                                                                                                                                                                                                                      Location/Qualifiers
102. 10649
/*tag= a
                                                                                                                                                                                                                    Dengue virus type 4 strain 2A DNA.
                                                                                                                             AAD53910 standard; DNA; 10649 BP
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/product= "|
939. .2423
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25, Conservative
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                                                                                                                                                                                                                                                                             Dengue virus
                                                                                                                                                                                     28-MAY-2003
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P-PSDB; AAW06590.
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12-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT49304;
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mutation
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                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses used as some as a service of simultaneous protection against infections. The present confer confer simultaneous protection against infections. The present conk sequence encodes dengue virus (DEN) 2/3-VP1 fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (B) 270 may the present confer premembrane protein (PM) and an envelope protein (B) from wildtrype DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2B; NS2B; NS3; NSAB, NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype; chimeric DSN-2/1 virus; chimeric DBN-2/2 virus; chimeric DBN-2/1 virus; chimeric ben-2/4 virus; chimeric dengue hoemorrhagic fever; fetal dengue haemorrhagic fever; dengue shock syndrome;
                                                                                                                                                                                                                                                                                                                                                            Gaps
are avirulent and immunogenic, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halstead SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
                                                                                                                                                                                                                                                                                                       Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                               Score 25; DB 4; Length 10717; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                           3; Indels
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             dengue viruses.
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                     Example 2; Page 203-219; 470pp; English
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97. .10272
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Kinney R, Trent DW;
             vaccinating against a range of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN (UYMA-) UNIV MAHIDOL AT SALAYA
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Best Local Similarity 89.3%;
Matches 25; Conservative
Chimeric flaviviruses that
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11-SEP-1997
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'note= "A>T mutation, causes Asp to Val substitution"
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                                                                                                                                                                                       PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection.
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/transl except (pos:643. .645, aa.Xaa)
/transl except (pos:1135. .1137, aa.Xaa)
/transl except (pos:1393. .1395, aa.Xaa)
/transl except (pos:2809. .2811, aa.Xaa)
/transl except (pos:2808. .2812, aa.Xaa)
/transl except (pos:2808. .9210, aa.Xaa)
/transl except (pos:2808. .9210, aa.Xaa)
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/note= "C>T mutation"
37. .10272
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nes 25; Conservative
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1997-052330/05
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Flavivirus, Dengue virus, DEN, vaccine, infection, virucidal, avirulent, immunogenic, viral disease, pharmaceutical, chimeric, ss.
                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
                                                                                                                                                                           /product= "DEN-2/1-VP1 fusion protein"
            Dengue virus (DEN)-2/1-VP1 chimeric cDNA
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                                                                                                                                   Location/Qualifiers
97. .10272
/*tag= a
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                                                                              Dengue virus; type I.
Dengue virus; type II.
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                          e
"G>A mutation, causes Gly to Asp substitution"
                                                                                                                                                  /*tag= h
/note= "G>C mutation, causes Gly to Ala substitution"
                                                                               "C>T mutation, causes Leu to Phe substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection.
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Kinney R, Trent DW;
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note= "C>T mutation'
                                                                                                             /*tag= g
/note= "C>T mutation'
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/note= "C>T mutation"
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1es 25; Conservative
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P-PSDB; AAW06591.
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Matches
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Bhamarapravati N;

Butrapet S, Gubler DL,

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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the companying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses are also used as immunogens of multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DBN-2, Plavi) flusion protein related to the invention. This fusion protein contains attenuated DBN-2 pbx-53v backbone confers immunogenes the non-structural protein (NS3) -250 and the premembrane protein (pxM) and an envelope protein (B) from wild-type DBN-1 16007 virus. (Updated on 11-SBP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 10723;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 4; Pred. No. 0.37; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 cccarcrcranancccrecreries 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.3%;
Matches 25; Conservative
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(first entry)
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01-NOV-2001
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AAD14614 standard; cDNA; 10723 BP

RESULT 9 AAD14614/c

(first entry)

(revised)

11-SEP-2003 01-NOV-2001

AAD14614;

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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated nonstructural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses uch as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present CDNA sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein cued for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region followed by a capsid protein (C) encoding region, followed by the region encoding non-coding region, followed by the region encoding non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gubler DL, Bhamarapravati N;
                                    Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 89.3%; Score 25; DB 4; Length 10723; Local Similarity 89.3%; Pred. No. 0.37; les 25; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                         /product= "DEN-2 16681 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 252-268; 470pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                            Kinney RM, Kinney CYH, Butrapet S,
Wild-type, virulent DEN-2 16681 cDNA.
                                                                                                                              Location/Qualifiers
97. .10272
/*tag= a
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ID AAD14606 standard; cDNA; 10723
                                                                                                                                                                                                                                                                                                             16-FEB-2001; 2001WO-US005142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                              Dengue virus; type II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-497162/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAE07986
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01-NOV-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence encodes dengue virus (DEN) 2/4-VP1 fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from wild-
                                   Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent; 
immunogenic; viral disease; pharmaceutical; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          premembrane/membrane protein (prM) and an envelope protein (E) from wil
type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric flaviviruses that are avirulent and immunogenic, useful for
vaccinating against a range of dengue viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Butrapet S, Gubler DL, Bhamarapravati N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.3%; Score 25; DB 4; Length 10723; Best Local Similarity 89.3%; Pred. No. 0.37; Matches 25; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                        /*tag= a
/product= "DEN-2/4-VP1 fusion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 CCCATCTTCAATATCCCTGCTGTTGG 277
Dengue virus (DEN)-2/4-VP1 chimeric cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                              Location/Qualifiers
97. .10272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD14608 standard; cDNA; 10723 BP
                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2000; 2000US-0182829P.
                                                                                                                                                                                                                                                                                                                                         .6-FEB-2001; 2001WO-US005142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinney RM, Kinney CYH,
                                                                                           Dengue virus; type II.
Dengue virus; type IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-497162/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAE07985
                                                                                                                                                                                                                                                                   WO200160847-A2
                                                                                                                                                                                                                                                                                                       23-AUG-2001
                                                                                                                                Chimeric.
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AAD14608/c
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Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; mutein; avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
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Dengue virus; type II

Location/Qualifiers replace(57, C) /*tag= b .10272

/*tag= a /product= "DEN-2 PDK-53 protein variant" replace (524, A)

replace (2055, C) replace (2579, G) /*tag=

à /*tag= g replace(5547, T) ତି replace (4018, C) replace (8571, C) replace (5270, replace (6599, /*tag= /*tag= /*tag=

WO200160847-A2.

23-AUG-2001

16-FEB-2001; 2001WO-US005142

16-FEB-2000; 2000US-0182829P

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Bhamarapravati N; Butrapet S, Gubler DL, Kinney RM, Kinney CYH,

WPI; 2001-497162/54. P-PSDB; AAE07987 Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.

Example 1; Page 276-292; 470pp; English.

The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the viruse are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present CDNA sequence encodes attenuated dengue-2 (DEN-2) PDK-53 virus protein variant used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1) co DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region followed by a capsid protein (C) encoding protein (E) encoding negion, followed by the region encoding non-coding region, followed by the region encoding non-coding region followed by the region encoding non-coding region.

The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attennation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses used as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4 Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/WN-PPI fusion protein related to the invention. This fusion protein contains DEN-2 16681 backbone and the premembrane/membrane protein (pzM) and an envelope protein (E) from West onless of the invention of the premembrane/membrane protein (pzM) and an envelope protein (E) from West onless of the invention of the premembrane protein (pzM) (Updated on 11-

Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

SEP-2003 to standardise OS field)

Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.

Example 6; Page 300-316; 470pp; English

Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;

WPI; 2001-497162/54.

P-PSDB; AAE07988

Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;

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                                                                                                                                                                Flavivirus, Dengue virus, DEN, vaccine, infection, virucidal, avirulent, immunogenic, viral disease, pharmaceutical, chimeric, ss.
                  Gaps
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  Score 25; DB 4; Length 10723; Pred. No. 0.37;
                  3; Indels
                                                                                                                                                                                                                                             /product= "DEN-2/WN-PP1 fusion protein"
                  0; Mismatches
                                                                                                                                                  Dengue virus (DEN)-2/WN-PP1 chimeric cDNA.
                                                304 cccarcrcrarararccracrarise 277
                                  1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                      AAD14609 standard; cDNA; 10756 BP
                                                                                                                                                                                                                                                                                           16-FEB-2001; 2001WO-US005142.
   89.3%;
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                                                                                                                                                                                                                              97. .10305
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                      /*tag= a
                  25; Conservative
                                                                                                                     (revised)
                                                                                                                                                                                       Dengue virus; type II. West Nile virus.
Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                             WO200160847-A2
                                                                                                                   11-SEP-2003
06-AUG-2003
01-NOV-2001
                                                                                                      AAD14609;
                                                                                                                                                                                                        Chimeric
                                                                        RESULT 13
                                                                               AAD14609/
ID AAD1
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us-10-085-944-1.rng

AAD14612 standard; cDNA; 10648 BP.

AAD14612,

AAD14612;

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                                                                                                                                                                                                                                                                                                                                                                        Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2B; NS3; NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; seroctype; chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome; DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain 16681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDK-53, a clone of infectious attenuated Dengue 2 virus strain 1668 also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
                                          ö
89.3%; Score 25; DB 4; Length 10756; llarity 89.3%; Pred. No. 0.37; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32 BP; 12 A; 7 C; 10 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     DEN-2 cloning/sequencing sense primer, D2-274.
                                                                                                  304 CCCATCTTCAATATCCCTGCTGTTGG 277
                                                                               1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US009209
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Best Local Similarity 85.7%;
Matches 24; Conservative
                                                                                                                                                                                                                  AAT75919 standard; DNA; 32
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                    Local Similarity
tes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9640933-A1
                                                                                                                                                                                                                                                                                              15-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                         AAT75919;
  Query Match
                                        Matches
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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN.1, DEN.2, DEN.3 and DEN.4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes wild-type, virulent dengue.4 (DEN.4) 1036 virus protein to DEN.4) are mosquito-borne flavivirus chimeras. Dengue virus types 1-4 (DEN.1 to DEN.4) are mosquitor followed by a capsid protein (C) encoding region followed by a capsid protein (C) encoding region followed by the region, an envelope protein (B) encoding region followed by the region encoding region. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Butrapet S, Gubler DL, Bhamarapravati N;
                                                                                                                                                             Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 10648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indela
                                                                                                                                                                                                                                                                                        /*tag= a
/product= "DEN-4 1036 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.4; DI
Pred. No. 1.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 cccarcirricagaarcccrecreries 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 373-389; 470pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                 Location/Qualifiers
102. .10265
                                                                                                                        Wild-type, virulent DEN-4 1036 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-2001; 2001WO-US005142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2000; 2000US-0182829P.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 85.7 tes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinney RM, Kinney CYH,
                                                                                                                                                                                                                   Dengue virus; type IV.
                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-497162/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE07991
                                                                                                                                                                                                                                                                                                                                                 WO200160847-A2
                                                                   11-SEP-2003
01-NOV-2001
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Gaps

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4; Indels

0; Mismatches

1 CCCATCTCNTCANNATCCCTGCTGTTGG 28

31 CCCATCTTTTCAGTATCCCTGCTGTTGG 4

g

Score 23.4; DB 2; Length 32; Pred. No. 0.74;

Search completed: August 3, 2004, 18:46:01 Job time : 155.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

August 3, 2004, 18:28:49; Search time 37 Seconds (without alignments) 419.963 Million cell updates/sec

US-10-085-944-1 28 Title: Perfect score:

1 cccatctcntcannatccctgctgttgg 28 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 segs, 277475446 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		df			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
п	25	89.3	2357	4	US-08-869-423-1	Sequence 1, Appl:
7	21.8	77.9	3381	٣	US-08-937-195-1	ų
٣		77.9	3381	e	US-08-937-195-2	7
4	21.8	77.9	3381	m	US-08-915-152-1	Sequence 1, Appl:
ស	21.8	77.9	3381	٣	US-08-915-152-2	7
9	21.8	77.9	3381	S	PCT-US96-07627-1	H
7	21.8	77.9	3381	S	PCT-US96-07627-2	7
æ	20.2	72.1	10718	m	US-08-325-426B-1	H
Q	18.8	67.1	5674	ч	US-07-807-043B-8	Sequence 8, Appl:
10	18.8	67.1	5674	Н	US-08-190-411A-1	H
11	18.8	67.1	5674	ч	US-08-299-849B-8	æ
12	18.8	67.1	5674	~	US-08-560-024-1	H
13	18.8	67.1	5674	~	US-08-142-368A-8	8
14	18.8	67.1	5674	ო	US-08-967-727-8	œ
15	18.8	67.1	5674	ო	US-08-037-230D-8	80
16	18.8	67.1	5674	4	US-09-583-850-8	8
11	18.8	67.1	5674	4	US-09-579-197-8	ω,
18	18.8	67.1	5674	4	US-09-404-026-8	æ
19	18.8	67.1	5674	4	US-09-312-464-8	œ
50	18.8	67.1	5707	~	US-08-472-809B-8	8
21	18.8	67.1	6345	~	US-08-472-809B-7	7
22	18.2	65.0	2917	~	US-08-437-607A-3	'n
23	18.2	65.0	3030	4	US-09-439-313-333	333,
24	18.2	65.0	3030	4	US-09-352-616A-333	333,
25	18.2	65.0	3030	4	US-09-232-149A-333	Sequence 333, App
56	18.2	65.0	3030	4	US-09-636-215-333	333,
27	18.2	65.0	3030	4	US-09-685-166A-333	333,

Sequence 333, App Sequence 1, Appli Sequence 136, App Sequence 136, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli
US-09-688-489-333 US-08-520-878B-40 US-08-520-878B-40 US-09-023-655-1316 US-08-389-668A-1 US-08-725-566-1 US-08-725-566-1 US-09-849-334-3 US-09-849-334-3 US-09-876-594-926 US-09-976-594-926 US-09-976-594-926 US-09-561-818A-7 US-09-561-818A-7 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-3 US-09-561-818A-1 US-09-561-818A-1
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3030 1664976 1514 1514 2238 2238 2238 19025 1310 5410 5410 5542 6204 1867
0.000000000000000000000000000000000000
60000000000000000000000000000000000000
18.2 17.6 17.6 17.6 17.6 17.2 17.2 17.2 17.2 17.2 17.2
22222222222222222222222222222222222222
0 000 000000

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Kochel, Tadeusz
APPLICANT: Forter, Kevin R.
APPLICANT: Raviprakash, Kanakatte
APPLICANT: Raviprakash, Kanakatte
APPLICANT: Raviprakash, Kanakatte
APPLICANT: Hoffman, Stephen L.
APPLICANT: Hayes, Curtis G.
TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
TITLE OF INVENTION: Neutralizing Antibodies
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: 24
CORRESPER: Naval Medical Res. & Dev. Cmd.
STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 8901 WISCOURING
CITY: Betheeda
STATE: Maryland
STATE: Waryland
STATE: Augustin
COUNTRY: U.S.A.
ZIP: 20889-5606
COMBUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALECATION DATA:
APPLICATION NUMBER: US/08/869,423
FLING DATE: 04-JUN-1996
FLING APPLICATION NUMBER: US 60/017,839
FLING DATE: 04-JUN-1996
ATORNEY/AGENT INFORMATION:
AMANE: Kalish, Daniel
REGISTRATION NUMBER: 33,599
REGISTRATION POR SEQ 1D NO: 1:
FELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-5642
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2357 base paire
TYPE: nucleic acid
STRANDEDNESS: single
                       Sequence 1, Application US/08869423
Patent No. 6455509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-869-423-1/c
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1260
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LOCATION: 2310
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LOCATION: 1
OTHER INFORMATION: /not
OTHER INFORMATION: sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: Den-2 PR159/S1
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                     STRAIN: Dengue virus
STRAIN: New Guinea C
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Prem and Envelope
MAP POSITION: 330-2446
UNITS: bp
PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
AUTHORS: Weight, P J
AUTHORS: Wright, P J
TITLE: Partial nucleotide sequence and deduced amino
TITLE: virus type 2, New Guinea C and PUO-218 strains
JOURNAL: J. Gen. Virol.
VOLUME: 69
PAGES: 1391-1398
DATE: DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.3%; Score 25; DB 4; Length 2357; 89.3%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Irie, K
AUTHORS: Mohan, P M
AUTHORS: Basaguri, Y
AUTHORS: Putnak, R
AUTHORS: Padmanabhan, R
TITLE: Sequence Analysis of Cloned dengue virus type
Patent No. 645509
TITLE: 2 genome (New Guinea-C strain)
JOURNAL: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Padmanabhan, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
AUTHORS: Yaegashi, T
AUTHORS: Vakharia, V N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vanie.
Page, K
Sasaguri, Y
'~hnv, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257-267
1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-869-423-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
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PEATURE:
NAME/KEY: misc feature
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note="Positions in the S1 strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEX: misc_feature

LOCATION: 1218

OTHER INFORMATION: /note= "G is replaced by A for OTHER INFORMATION: wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1762
OTHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Start of coding strand
sequence for Capsid."
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...
COCATION: 343
-..
COTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "A is replaced by N for OTHER INFORMATION: Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1260
OTHER INFORMATION: /note= "T is replaced by G
OTHER INFORMATION: Wild-Type sequence"
FLIANS CALLS

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIRASHIGE, KATE H.
REGISTRATION NUMBER: 4733-0003.20
TELEPHONE: (202) 887-0763
TELEPHONE: (202) 887-0763
TELERAX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: /note= "C is replaced
OTHER INFORMATION: Wild-Type sequence"
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single
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2. Application US/08937195; Patent No. 613651; Patent No. 613651; GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.; APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.9%; Score 21.8; DB 3; Length 3381; 82.1%; Pred. No. 0.75; tive 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
               NAME/KEY: misc_feature
LOCATION: 616
COCHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
                                                                                                                      NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 cccarcrrrraararcccrecreries 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCATCTCNTCANNATCCCTGCTGTTGG 28
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
RGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.:
TELECHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.1<sup>3</sup>
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 167-180
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -08-937-195-2/c
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NAMES, ADII INTOCATION: Anote= "GAG(coding for Glu) is OTHER INFORMATION: Anote= "GAG(coding for Glu) is OTHER INFORMATION: Areblaced by GAA(coding for Glu) for the wild-type DEN-2 PRISS OTHER INFORMATION: Areblaced by GAA(coding for Glu) for the wild-type DEN-2 PRISS OTHER INFORMATION: Actation= ([1])

FEATURE: NAMES/EX: misc_feature
INCATION: 1258.1260
OTHER INFORMATION: Anote= "GTG(coding for Val) is OTHER INFORMATION: Actation= ([1])
FEATURE: AMMES/EX: misc_feature
INFORMATION: Actation= ([1])
FEATURE: NAMES/EX: misc_feature
INCORMATION: Anote= "ATT(coding for Ile) is OTHER INFORMATION: Anote= "ATT(coding for Val) for the wild-type DEN-2 PRISS OTHER INFORMATION: Actation= ([1])
OTHER INFORMATION: Anote= "ATT(coding for Val) for the wild-type DEN-2 PRISS OTHER INFORMATION: Actation= ([1])
OTHER INFORMATION: Actation= ([1])
OTHER INFORMATION: Actation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 1927_.1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ({1})
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1 LABC_IEALURE
COCATION: 1 / Notes "Start of coding strand OTHER INFORMATION: sequence for Capsid"
FEATURE:
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OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 616
COTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
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sequence of Envelope"
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LOCATION: 343
LOCATION: 343
LOCATION: 343
LOCATION: GODING 8
OTHER INFORMATION: sequence for premembrane"
                                            STRAIN: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FRATURE:
                                                                                                                                                                                                                                        LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
*^^*ATTON: 2326
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LOCATION: 841
OTHER INFORMATION: /not
OTHER INFORMATION: seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
                 MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue v
linear
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DB 3; Length 3381;

77.9%; Score 21.8;

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US-08-915-152-2/C
Sequence 2, Application US/08915152
| Sequence 2, Application US/08915152
| Patent No. 615477 |
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: CLEMENN SUBUNIT VACCINE AGAINST DENGUE INFECTION
| TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: MORRISON & FOSENSTER |
| STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
| CITY: WASHINGTON |
| CITY: WASHINGTON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Start of coding strand
sequence for preMembrane"
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                                                                                                                                                                      /note= "G is replaced by A for
Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Start of coding strand
sequence for Capsid."
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                                                                                                                                                                                                                                                                                                                                                                               /note= "C is replaced by T for
Wild-Type sequence"
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Wild-Type sequence"
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    OTHER INFORMATION: Wild-Type sequence
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                                  FEATURE:

NAME/KEY: misc_feature
LOCATION: 1762
OTHER INFORMATION: Wild-'
PEATURE:
NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: Wild-'
OTHER INFORMATION: Wild-'
OTHER INFORMATION: Wild-'
FEATURE:
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LOCATION: 841
OTHER INFORMATION: /note:
OTHER INFORMATION: seque:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
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LOCATION: 2310
OTHER INFORMATION: /note
OTHER INFORMATION: Wild-
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: 616
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LOCATION: 343
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OTHER INFORMATION:
FEATURE:
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LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note="Positions in the SI strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PRI59 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= ([1])
                                                   ó
                                                   Gaps
                                                   ..
0
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APPLICANT: IVY, JOHN M.

APPLICANT: KAKANO, ELLEN

APPLICANT: CLEMENTS, DAVID

TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500

CITY: WASHINGTON

STATE: DC
                                                   IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: DC
COUNTRY: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
CONSTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/915,152
FILING DATE: 20-AGG-1997
CLASSIP COATE: 10-JUL-1995
CLASSIP COATE: 10-JUL-1995
FILING APPLICATION NUMBER: 29-959
FILING APPLICATION NUMBER: 29-959
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KARE H.
REGISTRATION NUMBER: 29-959
TELEFAX: (202) 897-1500
TELEFAX: (202) 897-1500
TELEFAX: 90-4030
TELEFAX: SCO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
TYPE: UNLOISE aingle
TYPE: TOWNICATION TOWNICATION
TYPE: TOWNICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "G is replaced by A for OTHER INFORMATION: Wild-Type sequence"
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2
Best Local Similarity 82.1%; Pred. No. 0.75;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                               208 CCCATCTTTTAATATCCCTGCTGTTGG 181
                                                                                                                       1 CCCATCTCNTCANNATCCCTGCTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08915152
Patent No. 6165477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1218
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LOCATION: 1260
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representing corrections to the wild type DEN-2 PR159 strain reported by Hahn(Citation #1)" / Citation= ([1])
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NUMBER OF SEQUENCES: 50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DSS/MS-DS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRATION SYSTEM: PC-DSS/MS-DS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRATION NUMBER: PCT/US96/07627
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE TARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORGANISM: Denque virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: misc feature
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Pred. No. 0.75;
0; Mismatches 5; Indels 0;
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LOCATION: group(103, 1940, 1991, 2025)
LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: reported by Hahn(citation #1)"
OTHER INFORMATION: reported by Hahn(citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1218
OTHER INFORMATION: /note= "G is replaced by A for OTHER INFORMATION: wild-Type sequence"
FEATURE:
                                                                                                NAME/KEY: misc_feature
LOCATION: 616
COTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
REATURE:
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
      /note= "Start of coding strand sequence for preMembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coding strand
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2326.
OTHER INFORMATION: /note= "Start of cod
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 CCCATCTTTTAATATCCCTGCTGTTGG 181
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; Sequence 1, Application PC/TUS9607627
; GENERAL INFORMATION:
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82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.13
Matches 23; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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DATE: 1988
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LOCATION: 1258-1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PRIS
OTHER INFORMATION: Strain(Citation #1)"
OTHER INFORMATION: /citation= [[1]]
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NAME/KEY: misc_feature
LOCATION: 1762_.1764
COTHEN INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PRISS OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: (citation #1)"
OTHER INFORMATION: (citation #1)"
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LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= {[1]}
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OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PRIS
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= [[1]]
   COUNTRY: Usa

ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-041-1995
FILING DATE: 10-041-1995
ATTORNEY/AGBNT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 4/33-0003.21
TELEPHONE: (202) 897-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for Capsid" FEATURE: NAME/KEY: misc_feature LOCATION: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: 1216..1218
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LOCATION: 1..3381
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APPLICATION NUMBER: PCT/US96/07627
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                       ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /not
OTHER INFORMATION: seq.
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LOCATION: 841
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LOCATION: 2326
                                                                                                                                                                                                                                                                                          Den-2 PR159/S1
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Virology
                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1..3381
                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
JOURNAL:
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TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
NUMBER OF SEQUENCES: 50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.9%; Score 21.8; DB 5; Length 3381; Best Local Similarity 82.1%; Pred. No. 0.75; Matches 23; Conservative 0; Mismatches 5; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE:
NAME/KEY: misc_feature
LOCATION: 1
COTHEN INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 841 - OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for Envelope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2326—
OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: Bequence for NS1"
AUTHORS: Hahn, Y.S.
JUURNAL: Virology
                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: /note= "C is replaced by T for
OTHER INFORMATION: Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Start of coding strand sequence for preMembrane"
                                       OTHER INFORMATION: /note= "T is replaced by G for OTHER INFORMATION: Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                /note= "A is replaced by N for
Wild-Type sequence"
                                                                                                   NAME/KEY: misc_feature
LOCATION: 1762_
OTHER INFORMATION: /note= "G is replaced by A
OTHER INFORMATION: Wild-Type sequence"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 CCCATCTTTTAATATCCCTGCTGTTGG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note
OTHER INFORMATION: seque
                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 841
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                       LOCATION: 2310
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-1
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PEATURE:
NAME/KEY: misc_feature
LOCATION: 11.5381
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PRISS
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12186..1280
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
PEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATION: 1762_.1764

COTHER INFORMATION: /note= "ATT(coding for Ile) is

OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159

OTHER INFORMATION: strain(citation #1)"

OTHER INFORMATION: /citation= ([1])

FRATURE:

NAME/KEY: misc_feature

LOCATION: 1927_.1929

LOCATION: 1927_.1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1927_..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PRIS9
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for NS1" PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Start of coding strand sequence for Capsid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 616
LOCHER INPORMATION: /note= "Start of coding strand
OTHER INPORMATION: sequence of Membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 841 OTHER INFORMATION: /note= "Start of codi OTHER INFORMATION: sequence of Envelope"
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Sequence 1. Application US/08190411A
Patent No. 5541104
GENERAL INFORMATION:
APPLICANT: Chen, Yachi Garin-Cheea, Pilar; Rettig, Wolfgang J.;
APPLICANT: Chen, Yachi Garin-Cheea, Pilar; Rettig, Wolfgang J.;
APPLICANT: Old, Lloyd J.
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: MONOCLONL ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1,
TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEFTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 5674;
                  CORRESPONDENCE AVENTION: Third and den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, TITLE OF INVENTION: Tumor Rejection Antigen Precursors, TITLE OF INVENTION: Tumor Rejection Antigen and UBes Thereof NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: Felie & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York City
STATE: New York City
STATE: New York City
STATE: New York
ZIE: 10022
COMPUTER: Babable Form:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: Mow York
STATE: New York
STATE: Now York
APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 1991122
CLASSIFICATION NUMBER: 07/764,364
APPLICATION NUMBER: 07/705,702
FILING DATE: 3-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1091
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REFERENCE/DOCKET NUMBER: 1UD 253.3
TELECOMMUNICATION NUMBER: 1UD 253.3
TELECOMMUNICATION NUMBER: 1UD 253.3
TELECOMMUNICATION NUMBER: 1UD 253.3
TELECOMMUNICATION NUMBER: 1UD 253.3
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-384
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.1%;
80.0%;
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CORRESPONDENCE ADDRESS:
ADDRESSES: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5674 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.01
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MAGE-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-807-043B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FU, Jianlin
APPLICANT: TAN, Boon-Haun
APPLICANT: TAN, Boon-Haun
APPLICANT: TAN, Eu-Hian
APPLICANT: TAN, Yin-Hwee
APPLICANT: TAN, Yin-Hwee
TITLE OF INVENTION: CINGAPORE STRAIN)
TITLE OF INVENTION: (SINGAPORE STRAIN)
NUMBER OF SEQUENCE: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON and VANDERHYE PC
                                                                                                                                Length 3381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 16-DEC-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10/18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                 Indels
                                                                                                                           ch 77.9%; Score 21.8; DB 5; 1 Similarity 82.1%; Pred. No. 0.75; 23; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA sequence corresponding to
MOLECULE TYPE: the genomic RNA of DENI-S275/90
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON and VANDERHYE PC
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIGGINIA
COUNTRY: USA
ZIP: 22201-4714
                                                                                                                                                                                                                                                                 208 CCCATCTTTTAATATCCCTGCTGTTGG 181
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STRAIN: S275/90
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08325426B Patent No. 6017535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/07807043B; Patent No. 5342774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 81..10268
                                                                                                                                                   Best Local Similarity
Matches 23; Conserv
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-2
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          -08-325-426B-1/c
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                                                                                                                                Query Match
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COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: MAGE-1 gene
US-08-299-849B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-560-024-1
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Patent No. 5612201

GENERAL INFORMATION

APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;

AURENTONE OF EGUENCES: 48

CORRESPONDENCES ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                              MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM OPERATING SYSTEM: PC-DOS
                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,411A
FILING DATE: 01-FEBRUARY-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
ATTORNEY AGENT INFORMATION:
ANAME: VACANT INFORMATION:
ANAME: VACANT NUMBER: 07/705,702
FILLING DATE: 23-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hanson, No. 5541104man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5354
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
TYRE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1897 crcarcrarcagaarcccrecrer 1921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MAGE-1 gene
                            ZIP: 10022
COMPUTER READABLE FORM:
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-299-849B-8
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GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1,
TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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Pred. No. 20;
                                                                                                                                                   OPERATING SIGLER: rc-Lucs
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/29,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFTCATION ATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 2-6-MARCH-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION NUMBER: 9-JULY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HAINSON, NO. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE (212) 838-3884
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
FINNORMATION FOR SED ID NO: 8:
FINNORMATION FOR SED ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1897 crcarcirgicagaarcccrdcrdr 1921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.1%;
Best Local Similarity 80.0%;
Matches 20; Conservative
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STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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18-06-977-727-8

Sequence 8, Application US/08967727

Sequence 8, Application US/08967727

Patent No. 6025474

Patent No. 6025474

GENERAL INFORMATION:

APPLICANT: daugler, B atrice; Van den Eynde, Beno t;

APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Nucleich Acid Molecules Coding For

TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

NUMBER OF SEQUENCES:

ADDRESSEE: Felfe & Lynch
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM
OPERATION SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION INTER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION NUMBER: PCT/US92/04354
FILING DATE: 2-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/84,364
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 07/705,702
FILING DATE: 33-MAY-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 33-MAY-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE DOCKET NUMBER: 10,705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 6886-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDESSEE: Felfe & Lynch
STRET: 805 Third Avenue
CITY: New York City
STATE: New York City
STATE: New York
ZIP: "10022
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.1%; Score 18.8; E
Best Local Similarity 80.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 5674 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: MAGE-1 gene
US-08-142-368A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Boon-Falleur, Thierry; Van den Bruggen, Thierry;
APPLICANT: Van den Eynde, Benc 1; Van Pel, Aline; De Dlaen,
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES. 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.1%; Score 18.8; DB 2; Length 5674; Best Local Similarity 80.0%; Pred. No. 20; Matches 20; Conservative 0; Mismatches 5; Indels 0
      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                            SOFTWARE:

SOFTWARE:

WORGENT APPLICATION DATA:

PAPLICATION NUMBER: US/08/560,024

FILING DATE:

CLASSIFICATION DATA:

PRICK APPLICATION DATA:

PRICK APPLICATION DATA:

APPLICATION NUMBER: US/08/190,411

FILING DATE: 0.FEBRUARY-1994

APPLICATION NUMBER: 037,230

FILING DATE: 26-MARCH-1993

PRIOR APPLICATION NUMBER: 07/0592/04354

FILING DATE: 22-MAY-1992

PRIOR APPLICATION NUMBER: 07/067,043

FILING DATE: 23-EMER-1991

PRIOR APPLICATION NUMBER: 07/067,043

FILING DATE: 23-EMER-1991

PRIOR APPLICATION NUMBER: 07/728,838

APPLICATION NUMBER: 07/728,838

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION NUMBER: 07/705,702

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION NUMBER: 07/705,702

FILING DATE: 23-MAY-1991

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-MAY-1991

APPLICATION NUMBER: 07/705,702

FILING DATE: 13-838-3844

INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:

LENGTH: S674 DASSE PAIRS

TYPE: MUCLEIC CACIG

SEQUENCE CHARACTERISTICS:

LENGTH: S674 DASSE PAIRS

TYPE: MUCLEIC CACIG

STRANDEDNESS: SINGIE

TOPOLOGY: 1 linear
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Patent No. 5925729
                                                                    COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MAGE-1 gene
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US-08-142-368A-8
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DB 2; Length 5674;

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Search completed: August 3, 2004, 19:52:12
Job time : 39 secs
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US-VB-037-230D-8

Sequence 8, Application US/08037230D

Patent No. 6235525

GENERAL INFORMATION:

APPLICANT: Van der Bruggen, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

NUMBER OF SEQUENCES: 30

CORRESSONDENCES: 30

CORRESSONDENCES: 30

CORRESSONDENCES: 30

CORRESSONDENCES: 30

CORRESSONDENCES: 30

CORRESSONDENCES: 30

CORPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: Wordgerfect

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 26-MARCH-1993

CLASSIFTCATION DATA:
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Pred. No. 20;
0; Mismatches
                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: 07/05/04354
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/708,038
FILING DATE: 23-MAY-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10D 5353
TELEBORNE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE THRACTERISTICS:
LENGTH: 5674 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1897 crcarcircicagaárcccrccrcr 1921
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APPLICATION NUMBER: US/08/967,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.1%;
Best Local Similarity 80.0%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MAGE-1 gene
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Gaps
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APPLICATION NUMBER: PCI/USSZ/U41534
PRICRA PAPLICATION NUMBER: PCI/USSZ/U41534
PRICRA APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRICRA APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRICRA APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRICRA APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRICRA APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANGON, NO. 6235525man D. REFERENCE/DOCKET NUMBER: 1UD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      LUD 5353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5674 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: MAGE-1 gene
US-08-037-230D-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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August 3, 2004, 18:40:54; Search time 158 Seconds (without alignments) 868.911 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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5.1.6
Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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28
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                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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	QI	US-10-085-944-1	US-10-247-960-2	US-10-027-632-281617	US-10-027-632-281617	US-10-437-963-62174	US-10-029-386-27304	US-09-864-761-27448	US-10-029-386-13604	US-10-437-963-53513	US-10-322-281-484	US-10-322-281-483	US-10-087-192-1870	US-09-814-353-1708	US-09-814-353-8061
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	Query Match Length DB	28	3381	691	691	2739	482	486	577	2301	6412	61396	98634	476	476
de ,	Query	89.3	77.9	68.6	68.6	67.1	66.4	66.4	66.4	66.4	66.4	66.4	66.4	65.0	65.0
	Score	25	21.8	19.2	19.2	18.8	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.2	18.2
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U	17	18.2	'n	3030		US-09-759-143-333	
υ	18	18.2	'n.	3030		US-09-780-669-333	333,
υ	19	8	5	3030		US-09-822-827-333	٠.
υ	20	8	5.	3030		US-09-232-880-333	•
υ	21	œ	ъ.	3030		US-09-895-793-333	٠.
υ	22	18.2	ď.	3030	თ	US-09-895-814-333	
U	23	ω.	ů.	3030	14	US-10-012-896-333	Sequence 333, App
U	24	ω.	'n.	3030	ษา	US-10-010-940-333	Sequence 333, App
O	25	ω.	ď.	3030	15	US-10-144-678A-333	Sequence 333, App
U	56	18.2	ů.	3030	12	US-10-294-025-333	Sequence 333, App
U	27	æ.	S.	77777	11	US-10-318-389-4	Sequence 4, Appli
	28	œ.	ω.	81826	12	US-10-175-523-197	Sequence 197, App
	59	۲.	m.	415	13	US-10-027-632-183225	Sequence 183225,
	30	7.	ë.	415	16	US-10-027-632-183225	Sequence 183225,
	31	7.	ë	1277	11	US-10-437-963-83170	Sequence 83170, A
	32	•	٠.	90798	11	US-10-318-819A-4	G)
	33	7.	ö	239	σ	US-09-864-761-26181	Sequence 26181, A
U	34	۲.	'n	353	11	US-09-864-408A-2719	Sequence 2719, Ap
υ	35	•	ς.	371	11	US-10-437-963-13942	Sequence 13942, A
	36	٠	ς.	410	σ	US-09-864-761-21296	Sequence 21296, A
	37	7.	ď	453	10	US-09-918-995-14536	Seguence 14536, A
	38	•	2	494	σ	US-09-864-761-4549	Seguence 4549, Ap
	39	7	2	999	0	US-09-864-761-9825	equence
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	7 7	•		١٥	1 4	10-027-632-15626	1 -
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						ALIGNMENTS	
RESULT	JLT 1	SULT 1					
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ภ์	Sequence	e 1, A	pplicat	Sequence 1, Application US/10085	001	35944	
	IDIICA RNEDAL	TNEOD	FUDITICATION NO. USZUGENEDAL INFORMATION:	102U1554	15A.		
۶ ´	OF TOO	ANT. W	Tang Man	7			
	PITIE	OF TNV	ENTION:	TITLE OF INVENTION: DETECTION	NO	OF DENGIE VIRUS	
	TIRE	EFFRE	ICE - 125	FILE REFERENCE: 12563-004001	;		
	URREN	T APPL	ICATION	NUMBER	, š	CURRENT APPLICATION NUMBER: US/10/085,944	
	URREN	T FILI	NG DATE	1: 2002	-06		
	PRIOR	APPLIC	ATION N	IUMBER:	60/	272,535	
	PRIOR	FILING	FILING DATE:	2001-03	٠ <u>.</u>		
	NUMBER OF		×				
	SOFTWARE:		FastSEQ f	for Windows	OWB	Version 4.0	
	SEQ ID NO	NO 1 H: 28					

Query Match
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 28; Conservative 0; Mismatches 0; Indels 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28 1 CCCATCTCNTCANNATCCCTGCTGTTGG 28 ઠે 엽

NAME/KEY: misc_feature; LOCATION: 9, 13, 14; COTHER INFORMATION: n = inosine US-10-085-944-1

ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Primer FEATURE:

TYPE: DNA LENGIH:

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Gaps

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RESULT 2 US-10-247-960-2/c

us-10-085-944-1.rnpb

Indels

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21; Conservative
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                Matches
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-22

PRIOR PLICATION NUMBER: US 60/199,676

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR PLICATION NUMBER: US 60/193,483

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR PLICATION NUMBER: US 60/167,363

PRIOR PLICATION NUMBER: US 60/167,363

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-10-20

PRIOR PLING DATE: 1999-09-20

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09
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                                                                                        APPLICANT: Hawaii Biotechnology Group, Inc.
APPLICANT: Peters, Iain
APPLICANT: Peters, Iain
APPLICANT: Coller, Beth-Ann
APPLICANT: McDoell, Michael
APPLICANT: Ivy, John
APPLICANT: Ivy, John
APPLICANT: Ivy, John
APPLICANT: Ivy, John
TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
TITLE OF INVENTION: AGAINST FLAVIVIRAL
TITLE OF INVENTION WINBER: 09/376,463
FRIOR FILING DATE: 1999-08-18
FRIOR FILING DATE: 1999-08-18
FRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 2
LENGIN: 3381
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Pred. No. 42;
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Publication No. US20020198371A1
GENERAL INFORMATION:
Sequence 2, Application US/10247960 Publication No. US20030175304A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.6%;
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Dengue virus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2
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Best Local Similarity
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US-10-027-632-281617
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APPLICANT: LA ROSSA, Thomas J.
APPLICANT: LA ROSSA, Thomas J.
APPLICANT: Ex Rossa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 62174
MANDER OF SEQ ID NOS: 204966
SEQ ID NO 62174
MANDER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                     Sequence 281617, Application US/10027632
| Publication No. US20030204075A9
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION NUMBER: US 60/218,006
| PRIOR FILING DATE: 2000-07-12
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/185,218
| PRIOR APPLICATION NUMBER: US 60/185,318
| PRIOR PILING DATE: 1999-11-23
| PRIOR PILING DATE: 1999-11-23
| PRIOR PILING DATE: 1999-09-08-09
| PRIOR PILING DATE: 1999-09-08-09
| PRIOR PILING DATE: US 60/146,002
Gaps
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Best Local Similarity 77.8%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 CCCAGCTCCTCATGTTCCCTGCTGATG 536
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 281617
LENGTH: 691
                                                                1 CCCATCTCNTCANNATCCCTGCTGTTG 27
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Publication No. US20040123343A1
GENERAL INFORMATION:
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Sequence 13664, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Renn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: PARSEL David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
UNDMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13604
LENGTH: 577
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 1.0
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: WINT: U07747.1, EVALUE 1.00e-15
OTHER INFORMATION: SWISSED IN FIT: P80192, EVALUE 8.00e-76
US-09-864-761-27448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annomax Sequence Listing Engine vers. 1.1
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-06-21
PRIOR PLING DATE: 2000-06-30
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ORGANISM: Homo sapiens
PEATURE:
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LENGTH: 486
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Sequence 27448 Application US/09864761

Sequence 27448 Application US/09864761

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: UNMER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/USO1/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27304, Application US/10029386

Sequence 27304, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: HANZEL, David R.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT PILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 27304

LENGTH: 482
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                                                                                                                   Length 2739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO CHR14.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: PB0192, WALLUE 9.00e-73
OTHER INFORMATION: EST HUMAN HIT: AA160611.1, EVALUE 4.00e-76
OTHER INFORMATION: NI HIT: AF251442.1, EVALUE 0.00e+00
                                                                                                                                                                                          Indels
                                                                                                                Query Match 67.1%; Score 18.8; DB 17;
Best Local Similarity 80.0%; Pred. No. 74;
Matches 20; Conservative 0; Mismatches 5;
; OTHER INFORMATION: Clone ID: PAT_MRT4530_63534C.1
US-10-437-963-62174
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ORGANISM: Homo sapiens
FEATURE:
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Gaps
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVEL Compositions and Methods in Cancer
FILE REFERENCE: 52945201000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 483
LENGTH: 61396
           Indels
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Sequence 1870, Application US/10087192

Publication No. US20020182586A1

Sequence 1870, Sequence 1870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.4%; Score 18.6; DB 17; Best Local Similarity 75.0%; Pred. No. 1.3e+02; Matches 21; Conservative 0; Mismatches 7;
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US-10-322-281-483
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Matches 21; Conservative
           21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
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           Matches
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; Bublication No. US20040126762A1
; GENERAL INFORMATION:
    APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; FILE REFERENCE: 52945201000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SEQ ID NO 484
; SEQ ID NO 484
; LENGTH: 6412
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                                                                                                                                                                                                                                               Query Match 66.4%; Score 18.6; DB 15; Length 577; Best Local Similarity 75.0%; Pred. No. 78; Matches 21; Conservative 0; Mismatches 7; Indels 0.
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P80192, EVALUE 1.00e-72
; OTHER INFORMATION: NT HIT: g114749516, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA160611.1, EVALUE 5.00e-76
US-10-029-386-13604
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US-10-437-963-53513
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
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Matches 21; Conservative
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US-10-322-281-484
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Best Local Similarity
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Length 476;

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; ORGANISM: Homo sapiens
US-09-814-353-8061
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                                           SUBJICATION NUMBER: US 60/21, 94

PUDIICANT: Let, John

APPLICANT: Let, John

APPLICANT: Let, John

APPLICANT: Lillie, James

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

THE REPERENCE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR PELICATION NUMBER: US 60/211,940

PRIOR PELICATION NUMBER: US 60/211,940

PRIOR PELICATION NUMBER: US 60/211,940

PRIOR PELICATION NUMBER: US 60/216,820

PRIOR PELICATION NUMBER: US 60/216,620

PRIOR PELICATION NUMBER: US 60/216,620

PRIOR PELICATION NUMBER: US 60/257,672

PRIOR PELICATION NUMBER: US 60/257,672
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US-09-814-353-8061/c

Sequence 8061, Application US/09814353

PUDIICALION NO. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Lillie, James

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR PLING DATE: 2000-05-21

PRIOR PLING DATE: 2000-05-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: US 60/220,661

PRIOR FILING DATE: 2000-07-27

NUMBER OF SEQ ID NOS: 22037

SOOTWARE: FastESE for Windows Version 4.0

SEQ ID NO 8061

LENGTH: 476
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                            Sequence 1708, Application US/09814353
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US-09-814-353-1708/c
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TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/18,006
PRIOR APPLICATION NUMBER: US 60/18,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/165,369
PRIOR APPLICATION NUMBER: US 60/165,369
PRIOR APPLICATION NUMBER: US 60/166,369
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09-38
PRIOR FILING DATE: 1999-09-08
NUMBER OF SEQ ID NOS: 325720
NUMBER PRIOR FILING DATE: 1999-08-08-08
NUMBER PRIOR FILING DATE: 1999-08-08-08
NUMBER OF SEQ ID NOS: 325720
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Query Match 65.0%; Score 18.2; DB 10;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 6;
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                                                                                                                               2 CCATCTCNTCANNATCCCTGCTGTTG 27
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Best Local Similarity 76.9
Matches 20; Conservative
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, ORGANISM: Human
US-10-027-632-256653
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n Ltd.	Search time 1253 Seconds	illion cell updates/sec			55026578			results predicted by chance to have a to the recare of the realt being printed,		Description	BB338318 BB338318 AQ517624 HS_5140_B BX109154 BXI09154 CC690447 OGXAB64TH
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	search, using sw model st 3, 2004, 18:26:44 ;	0S-10-085-944-1	IDENTITY NUC Gapop 10.0 , Gapext 1.0	27513289 seqs, 14931090276 residues	hits satisfying chosen parameters:	th: 0 th: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	emestba:* em_esthum:* em_esthum:* em_estfun:* em_estfun:* em_htc:* gb_est1:* gb_htc:* gb_est2:* gb_est3:* em_estfun:* em_gss_hum:* em_g	SUMMARIES	Query Match Length DB ID	68.6 287 10 BB338318 68.6 453 28 AQ517624 68.6 481 13 BX109154 68.6 577 29 CC690447
υ	OM nucleic - nucleic Run on: Augu	us core: 28	Scoring table: IDE	Searched: 275	Total number of hit	Minimum DB seq length: Maximum DB seq length:	Post-processing: Mi Ma Li	Database : 158, 21 158, 21 158, 21 158, 21 158, 22 158,		Result Que No. Score Mat	1 19.2 2 19.2 3 19.2 4 19.2

	Description	BB338318 BB338318 AQ517624 HS 5140 B BX109154 BXI09154 CC690447 OGXAB64TH
SUMMARIES	ID	c 1 19.2 68.6 287 10 BB338318 2 19.2 68.6 453 28 AQ517624 3 19.2 68.6 481 13 BX109154 4 19.2 68.6 577 29 CC690447
	DB	10 28 13 29
	Query Match Length DB ID	287 453 481 577
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ALIGNMENTS

BB33818 RIKEN full-length enriched, 10 days neonate cerebellum Mus musculus cDNA clone B930012N10 3' similar to U13152 Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, mRNA sequence.

DN BB33818.1 GI:9047081

SST.

Mus musculus (house mouse)

Nus musculus (house mouse)

Nus musculus (house mouse)

Mammalia: Eutheria: Rodentia: Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Mus.

CE 1 (bases 1 to 287)

RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kakat, J., Kikuchi, N., Kayosaw, H., Kojima, Y., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, X., Shibata, Y., Suzuki, H., Suzuki, H., Sakai, C., Kabanahi, F., Tominaga, N., Towanaka, I., Yano, R., Yasunishi, A., Takahashi, F., Tominaga, N., Toya, T., Tawanaka, I., Yano, R., Yoshida, K., Yoshida, A., Yoshida, M., Muramateu, M., and RESULT 1 BB338318/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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481 bp mRNA linear EST 07-FEB-2003 IMAGE: 873635, mRNA sequence.

BX109154 IG: 27835647
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                    Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
          genomic clone Plate=716 Col=21 Row=P, genomic survey sequence.
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Seg primer: SP6
Class: BAC ends
High quality sequence stop: 453.
Location/Qualifiers
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AQ517624.1 GI:4749772
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Hayashizaki, Y.

RIKEN Mouse ESTS (Konno, H., et al.)

Upublished (2000)

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Fax: 81-45-503-9216
Email: genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y. Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Okazaki, Y. and Hayashizaki, Y. (2xminci, P. and Hayashizaki, Y. (2xminci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 1944 (1999)
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cerebēllum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web site (http://genome.rtc.riken.go.jp) for
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AQ517624 HS_5140_B1_H11_SP6E RPCI-11 Human Male BAC Library Homo sapiens

DEFINITION

RESULT 2 AQ517624

Query Match

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AG063981 659 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-052019.F, genomic survey sequence.
AG063981
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ELOIN0432D03.b Endosperm_4 Zea mays CDNA, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
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                                                                                                                                                                                                                                                                                                       Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
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Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuyeen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-5735
                                                                                                                                                                                                                                                                                                     68.6%; Score 19.2; DB 29; 77.8%; Pred. No. 3.1e+03; ive 0; Mismatches 6;
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                                                                                                /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jlai@waksman.rutgers.edu
                            Location/Qualifiers
1. .577
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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo (dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo. "
Human UnigeneSet - RZPD3

Unpublished (2003)
Contact: Ina Rolfs
RZDD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAG9801044588.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZDD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response711bNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 110
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (cloneGrzpd.de) for further information. Seg primer:
M31, Primer sequence: TTPCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 bp DNA linear GSS 19-JUN-2003 Genomic survey sequence.
CC690447. GI:32095223
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
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Other_GSSs: OGXAB64TV
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952 bp DNA linear GSS 17-SEP-2003 PULOW63TDB ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTa0600K05, genomic survey sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/clone="zxwBTa06000005"
/clone lii="zw 0.6_1.0 KB"
/note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"
                                                                                                                                                /mol_type="genomic_DNA"
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/clone="zwmBMa0752D15"
/clone="xwcror:pBCSK-; Site 1: HinclI; 0.7-1.5 kb
methylation filtered genomic_DNA library"
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Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUIUW63TBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 68.6%; Score 19.2; DB 29; Length 952; Local Similarity 77.8%; Pred. No. 3.8e+03; es 21; Conservative 0; Mismatches 6; Indels 0
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
                                                                                                                              /organism="Zea mays"
                                      Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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Location/Qualifiers
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpese@gec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGEBIZOTV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0752D15, genomic survey sequence.
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1 (base) Lo 338)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Robbins, A., Bedell, J.A., Rohling, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other_GSSE: OG2BI20TH
                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Tel: 301-838-5843
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1. .659
/ organism="Pan troglodytes"
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                                          Pan troglodytes (chimpanzee)
Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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AG063981.1 GI:16615783
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RESULT 9 CNSO6EAJ/c LOCUS

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REFERENCE AUTHORS

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1018 bp DNA linear GSS 17-SEP-2003 PULJW63TBB ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTa0600K05, genomic survey sequence.
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CH261-33N7_Sp6.1 CH261 Gallus gallus genomic clone CH261-33N7,
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/mol_type="genomic DNA"
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COT selected genomic DNA library"
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1 (Dases 1 to 1139)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus Gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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1 Similarity 77.8%; Pred. No. 3.9e+03;
21; Conservative 0; Mismatches 6;
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Washington University School of Medicine
Bmail: submissions@wateson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
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Unpublished (2003)
Other GSSs: PUIJW63TDB
Contact: Cathy Whitelaw
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Gallus gallus
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Class: sheared ends.
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Zea mays
Zea mays
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Direct Submission

Submitted (06-SED-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 31057 BYRy cedex, FRANCE. (E-mail:

seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Rluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                         Sygosaccharomyces rouxii

Sygosaccharomyces rouxii

Sygosaccharomyce rouxii

Sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaese; Zygosaccharomycetes;

Saccharomycetales; Saccharomycetaese; Zygosaccharomycese.

I (bases 1 to 961)

Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

Genonitany,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,

Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

Peast species for molecular evolution studies
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                                                                        CNSO6EAJ 961 bp DNA linear GSS 17-JUN-2001 T3 end of clone AROAA020A08 of library AROAA from strain CBS 732 of 2990saccharomyces rouxli, genomic survey sequence.
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de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
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Pred. No. 3.8e+03;
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/mol_type="genomic DNA"
/mox.ref="texon:4956"
/clone="AR0A4020A08"
/clone=lib="AR0AAA"
/note="end : T3"
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FEBS Lett. 487 (1), 52-55 (2000)
20584718
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GSS.
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (basea 1 to 2314)
Straubberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
MCKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,
Gchnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                          / Organism="Gallus gallus"
/ organism="Gallus gallus"
/ wol_type="genomic DNA"
/ strain="Red Jungle Fowl"
/ db_xref="taxon:9031"
/ clone="GH261-33N7"
/ sex="female"="UCD01, inbred 256"
/ clone="lib="CH261"
/ note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
/ note="Vector: pTARBAC3.1; Site 1 : EcoRI; Site 2: CH261 Female Chicken library - For library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2314 bp mRNA linear HTC 19-NOV-2003 Mus musculus downstream of Stk11, mRNA (cDNA clone IMAGE:3982045), BC026893
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Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                    High quality sequence start: 145 High quality sequence stop: 618. Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 413)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NOI-ordap can come Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Emall: cgapbs-r@mail.nih.gov

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CONTACT: Robert Strausberg, Ph.D.

Emall: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 40 Row: i Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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                                                                                                                                                                 Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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/clone="IMAGB:3987045"
/tissue="IMAGB:3987045"
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/clone_lib="MCI (GAP_Lu29"
/lab_host="DH10B"
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Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6"
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
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BF723268.1 GI:12024270
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 445)

I (bases 2 to 445)

I (bases 2 to 445)

I (bases 3 to 445)

I (bases 4 to 445)

I (bases 4 to 445)

I (bases 4 to 445)

I (bases 3 to 445)

I (bases 3 to 445)

I (bases 4 to 445)

I (baseds, then cDNA was amplified by PCR using modified SWART primers The final cDNA was cloned in pAMP1 vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by Y. Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI.

Seq primer: - 40RP from Glbco

High county of the final of the final condition of 
                                                                                                                                                                                                                                                                                              /done="INGRE: 3971616"
/clone="INGRE: 3971616"
/tissue_type="branchial arches"
/dev_stage="embryo, 10.5 dpc"
/lab_host="BH10B (phage resistant)"
/lab_host="BH10B (phage resistant)"
/clone lib="Soares NNEBA branchial arch"
/clone lib="Soares NNEBA branchial"
/clone lib="Soares"
/c
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/dev stage="adult"
/lab_host="bHsalpha"
/clone_lib="Gastric Epithelial Progenitor"
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80.0%; Pred. No. 3.8e+03;
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Location/Qualifiers
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/db_xref="taxon:10090"
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/db_xref="taxon:10090"
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Seg primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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let strand of cDNA was synthesized with reverse transcriptese and olgo(dT) beads, then CDNA was amplified by PCR using modified SMART primers. The final cDNA was closed in pAMPI vector in annealing reaction with Uracil and Glycosylase (UDG). Library constructed by Y.Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 463) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 bp mRNA linear EST 14-JUN-2001 MR4-TN0112-080101-209-e05 TN0112 Homo sapiens CDNA, mRNA sequence. BI048424
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-TN0112-
080101-209-e05&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 463.
Location/Qualifiers
laser-captured isthmal cells from tox176 transgenic mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                 Length 445;
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                                                                                                                                                                                                                                                                              67.1%; Score 18.8; DB 14;
80.0%; Pred. No. 4e+03;
ative 0; Mismatches 5;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.0 Matches 20; Conservative
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Query Match 67.1%; Score 18.8; DB 12; Length 463; Best Local Similarity 80.0%; Pred. No. 4e+03; Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps දු පු

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Search completed: August 3, 2004, 19:50:54 Job time : 1259 secs

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August 3, 2004, 17:17:11 ; Search time 685.5 Seconds (without alignments) 1770.394 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                  3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           1 aatatgctgaaacgcgagagaaaccgcg 28
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		X51709 Dengue-2 vi	endue	engue	endue	uccura	AF469176 Dengue vi	engue	eng	D00346 Dengue viru	gue	engne	endne	engue	engue	engne	endue	engne	engne	endire	engue	engae	engue	5	engne	engne	engue	engne	engra	engue	engue	engue	endne	engue	endne	endre		A linear VRL 10-PEB-1999 1, partial, from a case of			es, no DNA stage; Flaviviridae,	am, S.K.
SUMMARIES		FLD2CPM2	AF360861	AF360862	AF360863	S55054 AF469175	AF469176	AF509530	AY04442 AP212496	DENZNGC	DENJAMA	AY152036S1	AY152044S1	AY152048S1	AY15205281	AY15205651	AY152064S1	AY152068S1	AY15207281	AY152080S1	AY152084S1	AY152088S1	AY15209281 AY15209681	AY152100S1	AY152104S1	AY15210851 AY15211251	AY152116S1	AY152120S1	AV15212451	AY15213281	AY152136S1	AY152140S1	AY152148S1	AY152152S1	AY152156S1	AY152160S1	ALIGNMENTS	342 bp RNA for capsid protein,			strand virus	g, T. and I
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Result No. S	1	н с	ım	4	ın v	۷ ٥	60	o (9.5	12	13	14	16	. 17	18	19	21	22	23	4 C	5 <u>6</u>	27	20 CV	30	31	32 6	3.6	32	0 r	38	6 E	4 c	4 4	43	4.	45		RESULT 1 FLD2CPM2 LOCUS DEFINITION	ACCESSION	VERSION KEYWORDS SOURCE	ORGANISM	REFERENCE AUTHORS

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PREFFFWMSSEGAMKHVQRIETWILRHFGFTINAAILAYTIGTTHFORALIFILLTAVA
PSWT"
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Flavivirus; Dengue virus group.
1 (Dases 1 to 840)
Uccategui, N. Y., Camacho, D., Comach, G., Cuello de Uzcategui, R., Holmes, E.C. and Gould, E.A.
Molecular apidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
Uccategui, Virol. 82 (Pt 12), 2945-2953 (2001)
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GVIVMLIPTAMAFRILTTRNGEPHMIVGRQEKGKSLLPKTEDGVNMCTLMAIDLGELCE
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Dengue virus type 2 isolate LARD1701 polyprotein gene, partial cds.
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Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Uzcategui,N.Y. and Gould,E.A.
Holmes,E.C. and Gould,E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 (UD, England
Location/Qualifiers
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/note="contains capsid, premembrane, and membrane
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AF360861.1 GI:18644123
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Dengue virus type 2 isolate LARD1432 polyprotein gene, partial cds.
AF360860
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Viruses, saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 840)
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/organism="Dengue virus type 2"
/mol_type="genomic RNA"
/strain="M2, isolated from case of dengue shock syndrome"
gene of three dengue-2 viruses isolated in Malaysia from patients with dengue haemorrhagic fever, dengue shock syndrome or dengue

    .>342
    'note="unnamed protein product; capsid protein, partial

                                                                                                                                                                                                                                                                                                                                                        Malaysia
See «M15075» and «M19197» for previously reported sequence. See
«X51708» and «X51710» for capsid protein sequences of M1 and M3.
Location/Qualifiers
                                                                                                                                                                                                                         Koh,C.L.
Direct Submission
Submitted (05-FEB-1990) Koh C.-L., University of Malaysia,
Department of Genetics and Cellular Biology, 5910 Kuala Lumpur,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road, Oxford OX2 6UD, England Location/Qualifiers
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Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Direct Submission
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; Pred. No. 0.14;
0; Mismatches 0; Indels
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|db_xref="taxon:11060"
                                                                                                 Nucleic Acids Res. 18 (7), 1904 (1990)
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Best Local Similarity 100.0%;
Matches 28; Conservative 0;
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Matches

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RESULT 4 AF360862

ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

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JOURNAL

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FEATURES

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KLFMALVAFLRFLTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLNILNRRRRTA
GVIIMLIPTAMAFHLTTRNGEPHMYGRQEKGKSLLPKTEDGVNMCTLMAIDLGELCE
DTITYKCPLLRQNEPEDIDCMCNSTSTWVTYGTCTTTGEHRREKRSVALVPHVGMGLE
TRTETWMSSEGAWKHVQRIETWILRHPGFAIMAAILAYTIGTTHFQRALIFILLTAVA
PSMT"
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Genetic determinants of dengue type 4 virus neurovirulence for mice
J. Virol. 67 (11), 6567-6575 (1993)
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Dengue virus type 4
Viruses; BSRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2319)
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/trānslation="MNNQRKKARGTPFNMLKRERNRVSTVQQLTKRFSLGMLQGRGPL
          Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Uzcategui,M.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Direct Submission
Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road,
Oxford OX2 (UD, England
Location/Qualifiers
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Location/Qualifiers
                              Flavivirus; Dengue virus group.

1 (Dases 1 to 840)
Uccategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R. Holmes, E.C. and Gould, E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela: evidence for in situ virus evolution and recombination J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
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/mol_type="genomic DNA"
/db_xref="taxon:11070"
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/organism="Dengue virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic RNA"
/isolate="LARD1996"
/db_xref="taxon:11060"
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Dengue virus type 2
Viruses; saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses; saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 840)
Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
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Dengue virus type 2 isolate LARD1996 polyprotein gene, partial cds.
AF360863
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Klfmalvaplrfltipptagilkrwgtikkskainvlrgfrkeigrmlnilnrrrta
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DTITYXCPLLRQNEPEDIDCMCNSTSTWVTYCTCTTTGEHRREKRSVALVPHVGMGLE
TRTETWMSSEGAWKHVQRIETWILRHPGFAIMAAILAYTIGTTHFQKALIFILLTAVA
PSMT"
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Uzcategui, N.Y., Camacho, D., Comach, G., Cuello de Uzcategui, R.,
Holmes, E.C. and Gould, E.A.
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    /note="contains capsid, premembrane, and membrane

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/organism="Dengue virus type 2"
/mol_type="genomic RNA"
/isolate="LARD1910"
          Pred. No. 0.13;
100.0%; Pred. ...
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/product="polyprotein"
/protein_id="AAL76290.1"
/db_xref="GI:18644126"
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Location/Qualifiers
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Dengue virus type 2
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       Local Similarity 100.
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Zhao, W.
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WILDERTULS I PPPAGILKRWGOLKKUKAL KITJGFRKETGRMLJAI LUNGRKRSTM
TLLCLI PTVARFHLSTROEDLAN WOLKKUKAL KITJGFRKETGRMLJAI LUNGRKRSTM
TLLCLI PTVARFHLSTROEDLAN WOLKHERGRPLLFFTTEGINKCTLIAMDLGERGED
TVTYECPLLWYTEPEDTDOWCALTASAWWYGTCTQSGERRRERRSKRSVALTPHSGKGEDE
TVTYECPLLWYTERGERAKHAQRYESMTLRNEGFALLAGFMAYNIGOTGIQRTVFFVLAMLVA
SABTWASSEGAMKHAQRYESMTLRNEGFALLAGFMAYNIGOTGIQRTVFFVLAMLVA
SYGRCVGVGRNBPFVEGSGGAMWUDSVLEHGGCVTTMAQGKPTLDFELLKTTAKEVAL
LRTYCLEASISNITTARRCPTGSEPYLKEEQDQQYICRRDVVDRGWGNGGGERGKGY
VTCARFSGGGLTLGDCFRGGIDFNEMILMKMKKTWTWLYRKQMPLDLPLPAAGADTSEV
HWNYKERMYTFRVPHARQDVIVLGSGGEAMISALTGATEVDSGGGRHMFAGHLKCKY
RMEKLRIKGMSYTMCSGKFSIDKEMATQHGTTVVKVKYEGAGAPCKVPIEIRDVNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF469175 20-FEB-2002
Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.
AF469175
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/protein id="AAL79017.1"
/b_xref="dg::18766555"
/translation="WINORKKAKTTPFNMLKRERNRVSTVQQLTKRFSLGMLGGRGPL
KLFMALVAFLRFLTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLNILNRRRRSA
                                                                                                                                                                                                                                                                                                                                                                                                                         KVVGRIISPTPFAENTNSVTNIELERPLÖSYIVIGVOOSALTLHWFRKGSSIGKWFES
TYRGAKRMAILGETAMDFGSVGGLLTSLGKAVHQVFGSVYTTMFGGVSWMVRILIGFL
VLMIGTNSRNTSMAMTCIAVGGITLFLGFTVQA"
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Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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1 (bases 1 to 2325)
Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and
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Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
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Submitted (16-JAN-2002) Department of Virology, The Military
Medical Institute of Guangzhou Military District, Dong Guanzhuang
Road 91, Guangzhou, Guangdong 5105407, China
Location/Qualifiers
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/country="China: Nanhai, Guangdong province"
/note="isolated from dengue haemorrhagic fever patient"
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                                                                                  'note="This sequence comes from Fig.
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/mol_type="genomic RNA"
/strain="GD24/93"
                gene="structural polyprotein"
. .2319
                                                             polyprotein"
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Pred. No. 0.13;
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                                                                                                                             /proteIn_id="AAB28474.1"
/db_xref="GI:432576"
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                                                           gene="structural
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Unpublished
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DTITYXCPLLRQNBEPBIDGWCNSTSTWVTYGTCTTGEHRREKRSYALVPHYGMGLE
PSHTETWMSSEGAWKHAQRIETWILBHPGFTIMAAILAYTIGTHRQRALIFILLAVA
PSHTRACIGISNBCARCHAQRIETWILBHPGFTIMAAILAYTIGTTHRQRALIFILLAVA
PSHTRACIGISNBCARCHAGGSGSWUDIVLEHGSCVTTMAKNUFTLDFELIKTEAKHPA
TLIKTYCIGAKTTTATRARCPFQGBBBLNBEQDKRFVCKHSWVDRGWCLEFGKGP
TIVTAMFTCKKAMRGGRVVQPBNLEYTIVITPHSGBRIAVGNDTGKHGKEIKVTPGSSI
TEAELTGYGTYTMGCSPFTGLDFNBWVLAQMBNKAMLVHRQWFLDLPLPWHPGADTGG
SNWIQKETLYTFKNBTAKQDVVSGSQEGANHTALTGATEIQMSGGNLEFTGHKKR
RHVGRLITVTPRYPARKQDVVSGSQEGANHTALTGATEIQMSGGNLEFTGHKCR
RHVGRLITVTPRYPAKQDVVSGSQEGGANTTALTGGGBGGSPCKIPFEIMDLER
RHVGRLITVTPRYPAKGDVYDSSQEGGANTTRIGGGGBGGGSCKLSWFKKGSSIGQMF
BTTMRGARRALISGGTAMPGGSLGGVFTSIGKALHQVFGAIYGAAFEGGSVGWTWKILIC
VVITWIGMNSRSTSLSVSLVLVGVVTLYLGVWVQA"
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TRTETWMSSEGAWKHAQRIETWILRHPGFTIMAAILAYTIGTTHFQRALIFILTAVA
PSMTMRCIGISNRDFVEGVSGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPA
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IVTCAMFTCKKNMEGKIVQPENLEYTIVVTPHSGEBHAIGNDTGKHGKEIKVTPQSSV
TEAELTGYGTVTIECSPRTGLDFNEMYLLQMKNAMLVHGQWFLDLPLPWLPGADTQG
SNWIQKETLVLKNPHAKKODVVVLGSQEGAMHALTGATEIQMSGNLLFTGHLKCR
LRMDKLQLKGNSYSWOTGKFKVVKEIAETQHGTIVIRVQYEGDGSPCKIPFEINDLEK
RYVLGRLITVNPIVTEKDSPVNIEAVPPFGDCYIIIGVEFGQLKLNWFKKGSSIGQMF
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Klfmalvaflrfltltpptagilkrmgtikkskainvlrgfrkeigrmlnilnrrrrsa
Gmiimliptvmafhlttrngephmivsiqekgksllfktedgvnmctlmamdlgelce
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Dengue virus type 2
Viruses, sRRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
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Ren, R.W., Fang, M.Y., Tian, X.D., Liu, J.W., Jiang, L.H., Lin, L.H. and
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Dengue virus type 2 strain GD08/98 polyprotein gene, partial cds.
AF469176.
AF469176.1 GI:18766556
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/country="China: Nanhai, Guangdong province"
/note="isolated from dengue haemorrhagic fever patient"
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/note="contains structural C, M and E proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 28; DB 14; Length 2
I Similarity 100.0%; Pred. No. 0.13;
28; Conservative 0; Mismatches 0; Indels
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/protein_id="AAL79018.1"
/db_xref="G1:18766557"
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/mol_type="genomic RNA"
/strain="GD08/98"
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DITTYRCELLROWEEDEDIDGE THE STATE AND THE STATE AND THE STATE BEATT BEATT
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Dengue virus type 2
Viruses, ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses, ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (Dases 1 to 2325)
Uzcategui, N. v., camacho, D., Comach, G., Cuello de Uzcategui, R.,
Molecategui, N. v., camacho, D., Comach, G., Cuello de Uzcategui, R.,
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
21571640
                                                                      AY04442 2125 bp 88-RNA linear VRL 10-FEB-2002 Dengue virus type 2 strain Mara3 polyprotein gene, partial cds.
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GVI IMLI PTAMAFHLTTRNGEPHMI VGRQEKGKSLL FKTEDGVNMCTLMA I DLGELCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .>2335
/codon_start=1
/product=in_id="AAL00888.1"
/brotein_id="AAL00888.1"
/db_xref="GI:L8643734"
/translation="MNNQRKKARSTPPNMLKRERNRVSTVQQLTKRFSLGMLQGRGPL
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Uzcategui,N.Y., Camacho,D., Comach,G., Cuello de Uzcategui,R.M.,
Holmes,E.C. and Gould,E.A.
Direct Submission
Submitted (09-UTL-2001) Flavivirus Group, CEH-Oxford, Mansfield
Road, Oxford OX1 35R, United Kingdom
Location/Qualifiers
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'product="premembrane/membrane protein"

    2325
    organism="Dengue virus type 2"

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/product="envelope protein"
/note="E; structural protein"
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'product="capsid protein"
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/strain="Mara3"
/db_xref="taxon:11060"
/country="Venezuela"
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                                                                                                                                            AY044442
AY044442.1 GI:18643733
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                                                                                                            DEFINITION
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AR232496
                                      AY044442
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Dengue virus type 2
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses; seRNA positive group.
1 (bases 1 to 2325)
Ren, Xu, Yu,F., Dongue virus group.
1 (bases 1 to 2325)
Ren, Xu, Yu,F., Dongue virus group.
1 (bases 2 to 2325)
Viruse 2 strain GD115/2001
Viruse 3 strain GD115/2001
Viruse 4 strain GD115/2001
ETTMRGAKRMAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWTMKILIG
VIITWIGMNSRSTSLSVSLVLVGIVTLYLGVMVQA"
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Ren,R., Yu,F., Dong,T., Wei,L., Hua,J., Yan,H. and Feng,C.
Burnect Submission
Submistical (06-MAY-2002) Microbiology Department, The Military
Medical Institute of Guangzhou Military District, Dongguanzhuang
Road, Guangzhou 510507, China
Location/Qualifiers
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Dengue virus type 2 polyprotein gene, partial cds.
AF509530
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mol_type="genomic RNA"

/strain="GD19/2001"

/specific host="dengue fever patient"

/db_xref="taxon:11060"
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100.0%; Pred. No. v..
0; Mismatches
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/codon_gtart=1
/product="polyprotein"
/protein_id="AAM34299.1"
/db_xref="G1:21070437"
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Best Local Similarity 100.
Matches 28; Conservative
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Matches 28; Conserv
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AUTHORS
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JOURNAL
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AF509530
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DENGLAMA 1469 bp 88-RNA linear VRL 18-MAR-2002 Dengue virus type 2 ARAC 8110827 polyprotein gene, partial cds. M15075
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SINMIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATELQMSSGNLLFTGHLKCR
LINDKLQLKGMSYSMCTGKKIJVKEI BAETQHGTT IT GVUGYEGDGSPCKIJ PFEINDLEK
RHVLGRLITVUPI VTPELDSPVNIEREPPFGDSYIJI GVUEPGQLKLMNFKKGSSIGQMF
ETTMRGAKRMAILGDTAMDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWTMKILIG
                        RHVLGRLITVNPIVTEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLNWFKKGSSIGQMI
ETTWRGAKRMAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWTWKILIG
VIITWIGMNSRSTSLSVSLVLVGVVTLYLGVMVQADSGC"
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Dengue virus type 2
Dengue virus type 2
Dengue virus type 2
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2469)
Deubel, V., Kinney, R.M. and Trent, D.W.
Nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue type 2 virus, Jamaica genotype
87701059
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RUJ MAJDARAFHLTTROMBEHMIVORGEKOKSLLFKTEDGVYMCTLAAIDLGBLCB
DUTIYYKCPLLRQNEBEDIDOWCTSTWYVYGTCATTGBHRBEKSVALVPHVGMGLE
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PSHTNRCIGISINRDVRGYSGGSWYDIVLBHGSGVTTWAKNRPTLDFBLTKTBAKQPA
TLRKYCIBALLTNTTESRCPTQGEBSLUKBEQDKRFLCKHSWVDRGWGNGCGLFGKGG
IVTCAMFTCKKNMEGKVVLPBNLBYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="polyprotein"
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ive 0; Mismatches
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1. .2469
/organism="Dengue virus type;/mol_type="genomic RNA"
/strain="ARAC 8110827"
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/note="genotype: Jamaica"
97. .>2469
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/product="capsid protein"
712. .936
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                                                                                                                                                                                                                                     861. .2345
/product="E protein"
2346. .>2357
/product="NS1 protein"
/note="amino end"
                                                                                                                                           363. .860
/product="prM protein"
                                                                                               21. .362
/product="C protein"
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/product="M protein"
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PSWTWRCIGISNRDFVEGVSGSWVDIVLEHGSCVTTWAKNKPTLDFELIKTEAKQPA
TLAKXCIBAALTNYTTDSRCPTQGESENEEQDREKVCKHSWYDRGWGGGLEGKGG
IVTCAMFTCKGMMKGKVVQEBNLEYIVITHSGEEHAVGNDTGKHGKEIKITPQSSI
TEABLTGYGTVTMESEPRTGLDFNEWYLLQMENKAMIVHRQWFLDLPLPWLPGADTQG
SNWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCR
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Viruses, saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses, saRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

(Analogue virus group.

GruenbergA., Woo, W.S., Biedrzycka, A. and Wright, P.J.

Bartial nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue virus type 2, New Guinea C and
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KLPWLVAPFLRFLTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLMILLNRRRRTA
GMIMLIPTVWAFHLTTRNGEPHMIYSRQEKGKSLLFKTEDGVNMCTLMAMDLGELCE
GMITYKCPFLRQNBPEDIDCWCNSTSTWTYGTCTTTGBHRREKSVALVPHVGMGLE
    PAT 20-DEC-2002
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Dengue virus type 2 gene for polyprotein, partial cds, strain:New
Guinea C.
                                                                                                                                                                                                                                                           Dengue nucleic acid vaccines that induce neutralizing antibodies Patent: US 6455509-A 1 24-SEP-2002;
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Kochel,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
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J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)
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fstrain="New Guinea C"
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    RNA
AR232496 2357 bp
Sequence 1 from patent US 6455509.
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/db_xref="GI:221231"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 2357
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/mol_type="genomic RNA"
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                                                   AR232496.1 GI:27274633
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Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial
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Flavivirus; Dengue virus group.
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KVVGRVISSTPLAENTNSTNIELEPPFGDSYIVIGYGNSALTLHWFRKGSSIGKMFE
STYGAKRMAILGETAMPFGSVGGLFTSLGKAVHQVPGSVYTTMFGGVSMMIRILIGF
LVLMIGTNGRNITSMATCIAVGGITLFLGFTVQADMGCVVSNGGRELKCGSGIFVGDN
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    >>2552
/note="contains core protein, matrix protein and envelope

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                                                                                                                                                                                                                                                                                                         Gaps
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Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
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                                                                                                                                   /product="nonstructural protein"
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/mol type="genomic RNA"
/isolate="bd.20_1998"
/db xref="taxon:11070"
/country="Puerto Rico"
                               937. .2421
/product="envelope protein"
2422. .>2469
'product="membrane protein"
                                                                                                                                                                                                                                                                                                                                                                      'note="acronym: DEN-4"
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Dengue virus type 4
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TUTYKCPLLVITEEDED INCOCKULTSTWANGTOTGGGGERREREKRSVALPHSGWGLET
RAETWMSSEGAWKTAQRUSSWILANGFALLAGFRAYNIGGTGIQRTVFFVLWMLVAP
SYGMCOVGUNDFVEGVSGGAWDLAGFRAYNIGGTGIQRTVFFVLWMLVAP
SYGMCOVGUNDFVEGVSGGAWDLAGFRAYNIGGTGIQRTVFFVLWMLVAP
LATYCIBASISNITTATACFOTGEPRYEEDDQOYICRRDVVDRGWGNGCGLFGKGGV
VTCAKFSCSGKITGNLVQIENLEYTVVVTVHNGDTHAVGNDTSNHGVTATITPRSPSV
BYALDFYCELLLDCEBRSGIDFREMILMKWKKTWLVHKQWFLDLEWTAGADTSEV
HWNYKERWYTFKVPHAKRODYTVLGSGGAMHSALAGATEVDSGDGHHMFAGHLKCKV
RREKLRIKGNSYTHCSGKFSIDKEMATGHOTTVVKWKYEGAGAPCKVPIEIRDVWKE
KVVGRVISSTPLAENTNSYTNIELEPPFGDSYIVJCGNSALTLHWGRGSSIGKMF
STYRGAKRMAILGETAWGSGTSLAGGATSKOVTHFGGSSGICKMF
STYRGAKRMAILGETAWGSTLEGFFYQADHGCVVSWSGRELKCGSGIFVVDN
VHTWTEQYKFQPESPARLASAILMAHKDGVCGIRSTTRLENVWWKQITNELN"
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/protein_id="AAN38327.1"
/db_xref="G1:28170822"
/translation="MNQRKKVNPPFNMLKRERNRVSTPQGLVKRFSTGLFSGKGPLR
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TLLCLIPTVMAFHLSTRDGEPLMIVAKHERGRPLLFKTTEGINKCTLIAMDLGEMCED
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Dengue virus type 4 D4.19_1998 polyprotein precursor, gene, partial
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Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Rio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennett, S. M., Hollmes, B.C., Chirivella, M., Rodriguez, D.M., Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O. Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico Piedras, PO Box 23366, San Juan 00931, Puerto Rico Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flavivirus; Dengue virus group.

1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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100.0%; Score 28; DB 14; Length 2552;
100.0%; Pred. No. 0.12;
ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 2552
/organism="Dengue virus type 4"
//old type="genomic RNA"
/isolate="D4.19 1998"
/db xref="taxon"11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
                                                                                                                        1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                                                                                                                              37 AATATGCTGAAACGCGAGAGAAACCGCG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                            AY152040
AY152040.1 GI:28170815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2552)
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                                                               28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
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Search completed: August 3, 2004, 19:08:57 Job time: 686.5 secs

OM nucleic - nucleic search, using sw model

August Run on:

3, 2004, 15:36:33 ; Search time 152.5 Seconds (without alignments) 779.997 Million cell updates/sec

US-10-085-944-2 28 Title: Perfect score:

1 aatatgctgaaacgcgagagaaaccgcg 28 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:* Database

geneseqn1990s:*
geneseqn2000s:*
geneseqn2001s:*
geneseqn2001ss:*
geneseqn2001ss:*
geneseqn2003s:*
geneseqn2003s:* 4.70.55 2.00.1 2.00.1 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn20048:*

SUMMARIES

		ф				
Result No.	Score	Query Match	Length	DB	, QI	Description
	28	100.0	28	7	ABX15698	Abx15698 Dengue vi
7	28	100.0	2357	7	ABX13740	Abx13740 Dengue vi
e	28	100.0	3381	7	AAT47666	Aat47666 Dengue vi
4	28	100.0	3381	7	AAX25114	Aax25114 Dengue vi
ស		100.0	10616	7	AAD53912	Aad53912 Dengue vi
9	28	100.0	10648	4	AAD14612	Aad14612 Wild-type
7	28	100.0	10648	4	AAD14613	Aad14613 Attenuate
80	28	100.0	10649	7	AAD53911	Aad53911 Recombina
6	28	100.0	10649	7	AAD53910	Aad53910 Dengue vi
10	28	100.0	10717	4	AAD14605	Aad14605 Dengue vi
11	28	100.0	10723	N	AAQ12787	Aag12787 Dengue 2
12	28	100.0	10723	~	AAT49303	Aat49303 cDNA sequ
13	28	100.0	10723	7	AAT49304	Aat49304 cDNA enco
14	28	100.0	10723	4	AAD14614	Aad14614 Dengue vi
15	28	100.0	10723	4	AAD14607	Aad14607 Wild-type
16	28	100.0	10723	4	AAD14606	Aad14606 Dengue vi
17	28	100.0	10723	4	AAD14608	Aad14608 Attenuate
18	28	100.0	10756	4	AAD14609	Aad14609 Dengue vi
19	26.4		10718	~	AAQ51476	o
20	26.4	94.3	10723	4	AAD14603	Aad14603 Dengue vi
21	26.4	94.3	10723	4	AAD14604	Aad14604 Dengue vi
22	26.4	94.3	10735	4	AAD14602	Aad14602 Attenuate
23	26.4	94.3	10735	4	AAD14601	Aad14601 Wild-type

-		Aad14610 Wild-type	Aad14611 Attenuate	Aaf88836 Green flu	Aac44997 Arabidops	Abg34003 Oligonucl	Abq34002 Oligonucl	Add46068 Human gen	Aac46148 Arabidops	Abl29849 Drosophil	Abl29848 Drosophil	Aaa82355 N. mening	Aaz36361 DNA encod	Abx16417 DNA encod	Aag22767 JEV Nakay	Abls0890 Japanese	Aav59364 Hepatitis	Abk87286 Hepatitis	Aca62469 DNA encod	Aaz36195 Nucleotid	Aai81993 Human pol
AAC68744	AAT75917	AAD14610	AAD14611	AAF88836	AAC44997	ABQ34003	ABQ34002	ADD46068	AAC46148	ABL29849	ABL29848	AAA82355	AAZ36361	ABX16417	AAQ22767	ABL50890	AAV59364	ABK87286	ACA62469	AAZ36195	AA181993
m	~	4	4	9	m	9	9	σ	m	4	4	m	ო	a	7	ო	~	ø	7	m	4
56	28	10699	10699	72	1083	765	765	28564	1008	3002	7264	449	1443	1443	4512	10976	12980	12980	12980	15065	333
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92	8	88	88	78	68	67	67	67	67	99	99	65	65	65.7	65	65	65	65	65	65.7	65
56	56	24.8	24.8	22	19.2	19	19	19	18.8	18.6	18.6	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.2
24	25	56	27	58	53	30	31	32	33	34	35	36	37	38	39	6	41	42	43	44	75
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ALIGNMENTS

RESULT 1

PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF; dengue haemorrhagic fever; virus; viral detection. Dengue virus detection PCR primer #2. ABX15698 standard; DNA; 28 BP. 31-MAR-2003 (first entry) ABX15698; ABX15698

Dengue virus

US2002155435-A1.

28-FEB-2002; 2002US-00085944. 24-OCT-2002.

01-MAR-2001; 2001US-0272535P

(WANG/) WANG W.

Wang W;

WPI; 2003-182625/18.

New dengue virus-specific primers, useful for reverse transcriptase-polymerase chain reaction assays, particularly for detecting or quantitating dengue virus in a sample.

Claim 28; Page 1; 6pp; English.

This invention relates to novel Dengue virus reverse transcriptase (RT) PCR primers which may be used to detect Dengue virus in a sample. Dengue virus is a member of the flavivirus family and causes diseases including dengue fever (DF) and dengue haemorrhagic fever. The invention also comprises a method for detecting and quantitating dengue virus. The dengue virus-specific primers of the invention are useful in reverse transcriptase-polymerase chain reaction assays, particularly for detecting or quantitating dengue virus in a sample. The present sequence represents a dengue virus specific RT-PCR primer used in the method of the invention

7; Length 2357;

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Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
                                             Matches
                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                 AAT47666
                                                                                                                             셤
                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses a pharmaceutical composition capable of inducing an immune response in a mammalian subject, comprising an immunogenic amount of a eukaryotic plasmid expression vector in pharmaceutical form, which includes the envelope and membrane (PreM) genes of a dengue type 1, 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of the family Plaviviridae and is a positive strand RNA virus encoding ten proteins. These genes are translated as a polyprotein which is cleaved by host and proteinsess. The virus envelope protein is a major antigen which can be targeted by neutralising antibodies. The membrane protein also appears on the virion surface and is required for proper processing of the envelope protein. Dengue viruses are transmitted primarily by the mosquito, Aedes aegyptii, and can lead to human illnesses ranging from cute undifferentiated fever to dengue hemorrhingic fever (DHF) and dengue shock syndrome (DSS). Secondary infections, with a different serotype, may lead to an immune enhancement phenomenon. The compositions of the invention are DNA vaccines which are injected into the animal as a technique of gene therapy. The composition is useful as a vaccine, particularly for inducing a protective immune response in mammalian subjecte against the dengue virus infection. The sequence presented is the chance of the inducing a protection. The sequence presented is
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pharmaceutical compositions containing dengue nucleic acids, useful as a vaccine, particularly for inducing a protective immune response in mammalian subjects against the dengue virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pharmaceutical; ds; immune response; immunogenic; envelope; membrane; PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen; mosquito; Aedes aegyptii; acute undifferentiated fever; dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS; immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
                                                                                        Gaps
                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the dengue virus type 2 (Den 2) structural gene genome segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Науев СС;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;
                                         100.0%; Score 28; DB 7; Length 28; 100.0%; Pred. No. 0.0052;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kochel IJ, Porter KR, Raviprakash K, Hoffman SL,
                                                                                                                                                                                                                                                                                                                                                                                                   Dengue virus type 2 structural gene genome segment.
Sequence 28 BP; 11 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                      0; Mismatches
                                                                                                                             1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                    1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 17-20; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00869423.
                                                              Local Similarity 100.0%; es 28; Conservative C
                                                                                                                                                                                                                                                                          ABX13740 standard; DNA; 2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0017839P
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structural gene; virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USNA ) US SEC OF NAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-066244/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dengue virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6455509-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-2002
                                                                                                                                                                                                                                                                                                                   ABX13740;
                                             Query Match
                                                                                    Matches
                                                                                                                                                                                                                                   RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1 shows 4 differences from the wild-type DEN-2 PR159. This results in a conservative mutation in domain B of S1 that may be involved in the attenuation of this small-plaque, temp.-sensitive variant. The CDNA encodes the capsid, pre-membrane, envelope and NS1 proteins (AAM09409) of the virus. The clone can be used to express recombinant secreted polypeptides, comprising portions of the envelope protein (esp. domain B, Gly296-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47657 and
                                                                                                                                                                                                                                                                                                                                                         /-rag= a
/note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
is GAA (Glu) in wild-type PR159"
1258. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= b
note= "codon GTT (Val) at position 1258-1260 of PR159/S1
s GTG (Val) in wild-type PR159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
is ATT (Ile) in wild-type PR159"
1927. .1929
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
is AGT (Ser) in wild-type PR159"
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sub:unit vaccine against flavivirus infection - contg. recombinant envelope protein in secretable form, used for immunising against
                            ö
                                                                                                                                                                                                                                                                                            DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss
                           0; Indels
                                                                                                                                                                                                                                                                Dengue virus serotype 2 PR159/S1 mutant sequence.
100.0%; Score 28; DB 7;
100.0%; Pred. No. 0.009;
ive 0; Mismatches
                                                         1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                     60 AATATGCTGAAACGCGAGAAACCGCG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3A-D; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                      Jocation/Qualifiers
                                                                                                                                                            AAT47666 standard; cDNA; 3381 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ivy JM, Nakano E, Clements D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00448734.
95US-00488807.
95US-00500469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    762. .1764
                                                                                                                                                                                                                    (revised)
(first entry)
                           28; Conservative
                                                                                                                                                                                                                                                                                                                         Dengue virus; serotype 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flavivirus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-020938/02.
P-PSDB; AAW09409.
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9637221-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0-JUL-1995;
                                                                                                                                                                                                                    17-OCT-2003
19-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-1996
                                                                                                                                                                                         AAT47666;
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This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This strain served as the source for DEN-2 genes used in the invention. A vaccine for protecting against flavivirus infection comprises a dimeric 80% E protein that has been secreted as a recombinant protein from a cukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E. The dimeric truncated E is formed: (1) by directly linking 2 tandem copies of 80% E via a flaxible tether; (2) via the formation of a leucine zipper companion through the homodimeric association of 2 leucine zipper helices each fused to the C-terminus of a 80% E molecule; or (3) via the formation of a non-covalently associated four-helix bundle domain formed upon association of two helix-turn-helix moieties attached to the C-terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are efficiently secreted by recombinant cells, are easier to purify than intracellular proteins, and generate a high titer neutralising antibody cresponse. The method is generally applicable to flaviviruses, in particular dengue viruses such as DEN-2, where 80% E comprises amino acids 1.395 of DEN-2 E. The products can also be used for diagnosis of infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric 80%E protein, useful for protecting against flavivirus, especially dengue
AAT47703-04) and Drosophila, for use in subunit vaccines against viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
                                                                                                                                          ö
                                                                                                Length 3381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
                                                       Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcdonnell M, Harada KE;
                                                                                                Score 28; DB 2;
Pred. No. 0.0094;
                                                                                            / Match 100.0%; Score 28; DB Local Similarity 100.0%; Pred. No. 0.0 nes 28; Conservative 0; Mismatches
                                                                                                                                                                             1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                                                                                                                                                                   40 AATATGCTGAAACGCGAGAGAAACCGCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3A-D; 60pp; English.
                                                                                                                                                                                                                                                                                                                     AAX25114 standard; cDNA; 3381 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coller BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US015447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00904227
                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dengue virus; serotype 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-153454/13.
P-PSDB; AAY05522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ivy JM, Peters ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2003
05-JUL-1999
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                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                              RESULT 4
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DB 2; Length 3381;

100.0%; Score 28;

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                                                                                                                                          Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds
             Gaps
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0
                                                                                                                                                                                              product= "DEN4 strain rDEN2/4delta30 protein"
             Indels
                                                                                                                                                                                                                                                                 "Membrane precursor protein"
                                                                                                                                                                                                              *tag= c
product= "Anchored capsid protein"
Pred. No. 0.0094;
                                                                                                                                                                                                                                    *tag= b
product= "Virion capsid protein'
                                                                                                                            Dengue virus type 2 strain rDEN2/4delta30 DNA.
                                                                                                                                                                                                                                                                                                             "Envelope protein"
                                                                                                                                                                                                                                                                                       "Membrane protein
   100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "NS4B protein"
|561, .10260
                                                                                                                                                                                                                                                                                                                                                                                product= "NS2B protein"
                                                                                                                                                                                                                                                                                                                                                         product= "NS2A protein"
                                                                                                                                                                                                                                                                                                                                                                                                                             "NS4A protein'
                                                                                                                                                                                                                                                                                                                                                                                                     product = "NS3 protein"
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                                                                                                                                                                                                                                                                                                                                   "NS1 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "2K protein"
826. .7560
                                     Location/Qualifiers
97. .10263
                                                                                AAD53912 standard; DNA; 10616 BP
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*tag= k
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*tag= i
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*tag= 1
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'product= '
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product= '
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/product=
                                                                                                                                                                                                                                                                                               . .2421
                                                                                                             (first entry)
                                                                                                                                                                                                                                                   . 936
      Best Local Similarity 100.8
Matches 28; Conservative
                                                                                                                                                                                       *tag= a
                                                                                                                                                                                                                                                                          2. .936
                                                                                                                                                                                                                                                                                                                                   product=
                                                                                                                                                                                                                            .396
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                                                                                                                                                         Dengue virus
                                                                                                             28-MAY-2003
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AAD53912
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The present invention relates to novel mutated flaviviruses comprising a phenotype in which the viral genome is modified by introduction of a mutation, singly or in combination, taken from mutations pearing Vero adaptation mutations, putative Vero cell adaptation wintations of dengue type 4 virus (DEM4) or mutations known to attenuate dengue type 4 virus. The methods and compositions known to attenuate useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and jor treatment of dengue virus robenz/4delta30 DNA
                                                                                                                         New mutated flavivirus, useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                            Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "DEN-4 1036 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATATGCTGAAACGCGAGAGAAACCGCG 163
                                                                                                                                                                                       Disclosure; Page 135-138; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
            (USSH ) US DEPT HEALTH & HUMAN SERVICES (BLAN/) BLANEY J E.
                                                         Hanley KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
102. .10265
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wild-type, virulent DEN-4 1036 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD14612 standard; cDNA; 10648 BP.
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(first entry)
                                                         Murphy BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinney CYH,
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                                                                                    2003-120809/11.
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P-PSDB; AAE07991.
                                                                                  WPI; 2003-120809/
P-PSDB; AAE35314.
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                                                       Whitehead SS,
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01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flavivirus;
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AAD14612
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요
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Bhamarapravati N;

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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a paramaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes will-type, virulent dengue-4 (DEN-4) 1036 virus protein used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1) to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region followed by a capsid protein (C) encoding region, premembrane/membrane protein (PM) encoding region, an envelope protein (B) encoding region, followed by the region encoding non-coding region, followed by the region encoding region of contains and protein (R) encoding region, followed by the region and envelope protein (B) encoding region, followed by the region and envelope protein (B) encoding region, followed by the region and envelope protein (B) encoding region followed by the region and envelope protein (B) encoding region followed by the region and envelope protein (B) encoding region, followed by the region and envelope protein (B) encoding region followed by the region and envelope protein (B) encoding region followed by the region and envelope protein (B) encoding region followed by encoding region encoding enveloped the protein (B) encoding region followed by enveloped by encoding enveloped by the region encoding enveloped by the region encoding enveloped by env
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structural proteins (NSI-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                    Example 3; Page 373-389; 470pp; English
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replace(7546,
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Best Local Similarity 100.0
....hes 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD14613;
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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses alicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines concer simultaneous protection against infections. The present cDNA sequence encodes attenuated dengue-4 (DEN-4) PDK-48 virus protein variant used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region, followed by a capsid protein (C) encoding region, premembrane/membrane protein (prM) encoding region, an envelope protein (E) encoding region, followed by the region encoding negion. DEN-4 PDK-48 virus primary dog kidney (PDK) cells concaing region. DEN-4 PDK-48 virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                 Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
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                                                                                                                                                                                                            Butrapet S, Gubler DL, Bhamarapravati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10648 BP; 3294 A; 2214 C; 2807 G; 2333 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "DEN4 strain rDEN4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant dengue virus type 4 strain rDEN4 DNA.
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                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 397-413; 470pp; English
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                                                                                                     16-FEB-2001; 2001WO-US005142.
                                                                                                                                      16-FEB-2000; 2000US-0182829P.
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/*tag= a
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Best Local Similarity 100.
Matches 28, Conservative
                                                                                                                                                                                                            Kinney RM, Kinney CYH,
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P-PSDB; AAE07992.
                                 WO200160847-A2
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                                                                    23-AUG-2001
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ઠે 셤

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New mutated flavivirus, useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection.
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                                                                                                                                                                 "Membrane precursor protein"
                                      "Anchored capsid protein"
                                                                                                  "Virion capsid protein
                                                                                                                                                                                                                                                                                     product= "Envelope protein
                                                                                                                                                                                                                           "Membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 131-132; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "NS4A protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product= "NS2B protein"
524. .6377
                                                                                                                                                                                                                                                                                                                                                                                                             product= "NS2A protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NS4B protein'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product= "NSS protein"
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product= "NS1 protein"
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7563. .10262
'*tag= n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanley KA;
                                                                                                                                                                                                                                                                                                                                                                    3480. .4133
/*tag= h
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*tag= i
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                                                                                                                                                                                                                                                                                                          424. .3479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .7562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378. .6758
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product= "
39. .2423
                                                                                                                                                            product=
102. .440
(*tag= c
/product=
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                                                            02. .398
                                                                                                    product=
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                                                                             *tag= b
                                                                                                                        41. .938
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P-PSDB; AAE35313.
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Kinney RM, Kinney CYH, Butrapet S, Gubler DL,
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                                                                                                                                                                                                     Local Similarity 100.0
les 28; Conservative
                                       Whitehead SS, Murphy BR,
                                                                                                                                                                                                                                                                                                                                                      Dengue virus; type II.
Dengue virus; type III.
                                                                                                                                                                                                                                                                                                   (revised)
                                                    WPI; 2003-120809/11.
                                                            P-PSDB; AAE35312
                                                                                                                                                                                                                                                                                                                                                                                                                   W0200160847-A2
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01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                     Chimeric.
                                                                                                                                                                                               Query Match
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                                                                                                                                    Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.
                   Gaps
                   ö
     Query Match 100.0%; Score 28; DB 7; Length 10649; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 28; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                             'product= "Membrane precursor protein"
                                                                                                                                                                                               *tag= c
product= "Anchored capsid protein"
                                                                                                                                                                                  'product= "DEN4 strain 2A protein'
                                                                                                                                                                                                                         product= "Virion capsid protein"
                                                                                                                                                                                                                                                                 product= "Membrane protein"
                                                                                                                                                                                                                                                                                    product= "Envelope protein"
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                                                                                                                                                                                                                                                                                                                                                                                        product= "NS4A protein"
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/product= "NS4B protein"
                                                                                                                                                                                                                                                                                                                           product= "NS2A protein"
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6378. .6758
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product= "NS1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                           product= "2K protein"
                                                                                                                                                             Location/Qualifiers
102. .10649
                                                                                                                       Dengue virus type 4 strain 2A DNA
                                                                              AAD53910 standard; DNA; 10649 BP
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                                                                                                         (first entry)
                                                                                                                                                                                         02. .440
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                                                                                                                                                Dengue virus
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                                                                                           AAD53910,
                                                                 RESULT 9
                                                                       AAD53910
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The present invention relates to novel mutated flaviviruses comprising a phenotype in which the viral genome is modified by introduction of a mutation, singly or in combination, taken from mutations from recombinant virus bearing Vero adaptation mutations, putative Vero cell adaptation mutations of dengue type 4 virus (DEN4) or mutations of the invention are useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and growth characteristics of dengue virus saccines for the prevention and/or treatment of dengue virus infection. The present sequence is Dengue virus type 4 strain 2A DNA
                                                                                                                                                                                                                                                                                                                                                                               New mutated flavivirus, useful for fine tuning the attenuation and growth characteristics of dengue virus vaccines for the prevention and/or treatment of dengue virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhamarapravati N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 28; DB 7; Length 10649; 100.0%; Pred. No. 0.011; 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AATATGCTGAAACGCGAGAAAACCGCG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dengue virus (DEN)-2/3-VP1 chimeric cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 123-126; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES. (BLAN/) BLANEY J E.
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                                                                                                                                                                                             Hanley KA;
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97. .10266
/*tag= a
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22-MAY-2001; 2001US-0293049P.
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us-10-085-944-2.rng

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DHF; DSS; 88.
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11-SEP-1997
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                                                                                                                                                                   FR2654113-A.
   mat_peptide
                                                     mat_peptide
                                                                                                  mat_peptide
                                                                                                                                                                                                  10-MAY-1991
                                                                                                                                                                                                                                                                                                                                    Vincent D;
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AAT49303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural genes of the virus are used as econd flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/3-VP1 fusion protein related to the invention. This fusion protein contains attenuated DEN-2 DEN-53V backbone comprising a valine at the non-structural protein (N3)-250 and the premembrane/membrane protein (PPM) and an envelope protein (E) from wildtype DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 100.0%; Score 28; DB 4; Length 10717; Local Similarity 100.0%; Pred. No. 0.011; es 28; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 AATATGCTGAAACGCGAGAGAAACCGCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                  Example 2; Page 203-219; 470pp; English.
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712. .936
/*tag= b
/product= "M protein"
937. .2421
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2422. .3477
/*tag= d
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3478. .4131
/*tag= e
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product= "NS2A"
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/product= "NS3"
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/*tag= g
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/*tag= f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dengue 2 virus genome.
WPI; 2001-497162/54.
P-PSDB; AAE07984.
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21-NOV-1991
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Matches
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Detection and identification of Flaviviridae in biological sample - by amplifying consensus sequence then hybridisation opt. followed by typing, e.g. sequencing amplified prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dengue 2 virus is an example of a member of the Flaviviridae which can be identified using the probe pair of the invention. A species-specific sequence can be amplified using the claimed oligonucleotides as primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses which can be identified include Japanese encephalitis virus and yellow fever virus. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3; NSAB, NSS, PDK-53; quadravalent vaccine; immunity; sercetype; chimeric DEN-2/3 virus; chimeric DEN-2/3 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
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Best Local Similarity 89.3%; Pred. No. 0.011;
Matches 25; Conservative 3; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "DEN-2 polyprotein
/transl_except(pos:9208. .9210, aa:Xaa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AATATGCTGAAACGCGAGAAACCGCG 28
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97. .10272
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                                      *tag= h
product= "NS4a"
                                                                                                                                                  product= "NS4B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 24pp; French
                                                                                                                                                                                                                                           'product= "NS5"
                                                                                                                                                                                                                                                                                                                                                                                                                                 89FR-00914724.
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/*tag= j
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.6825
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/*tag= i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR
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P-PSDB; AAR13166.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                             This sequence encodes the polyprotein from Dengue 2 virus, strain 16681. The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NSS proteins. A clone of this wildtype viral sequence, PDK -53, may be used in the production of a quadravalent vaccine which provides immunity against all four serotypes of dengue virus. The vaccine a climeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to protect against infection by all four serotypes of dengue virus, DEN-1, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the recombinant protein products of the DNA constructs which are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2B; NS2B; NS3; NS4B, NS5 PDK-53; quadravalent vaccine; immunity; serotype; chimeric DSN-2/1 virus; chimeric DBN-2/3 virus; chimeric DBN-2/4 virus; dengue haemorrhagic fever; dengue shock syndrome;
                                                                                                                                                                                                               PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                              Gubler DJ, Halstead SB;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 28; DB 2; Length 10723; 100.0%; Pred. No. 0.011; o; Indels 0, Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
 /note= "Xaa = unknown amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 AATATGCTGAAACGCGAGAGAAACCGCG 163
                                                                                                                                              Chang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES (UYMA-) UNIV MAHIDOL AT SALAYA.
                                                                                                                                                                                                                                                          Claim 23; Page 107-121; 261pp; English
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Synthetic.
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                                                                                                                                             Bhamarapravati N, Butrapet S,
Kinney R, Trent DW;
                                                                  96WO-US009209.
                                                                                      95US-00483292
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                                                                                                                                                                               WPI; 1997-052330/05.
                                                                                                                                                                                         P-PSDB; AAW06590
                      WO9640933-A1
                                                                 16-JUN-1996;
                                                                                       07-JUN-1995;
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DHF; DSS; 88
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12-SEP-1997
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Best Local S:
Matches 28
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mutation
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This sequence encodes the polyprotein from an attenuated derivative of Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The polyprotein comprises the capsid, prM, M. E. NSI, NS2A, NS2A, NS3, NS4A, NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the production of a quadravalent vaccine which provides immunity against all four serotypes of dengue virus. The vaccine also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to protect against infection by all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the recombinant protein products of the DNA constructs which are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
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"A>T mutation, causes Asp to Val substitution"
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"G>A mutation, causes Gly to Asp substitution"
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"G>C mutation, causes Gly to Ala substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C>T mutation, causes Leu to Phe substitution"
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*tag= a
product= "DEN-2 attenuated_polyprotein
                                                        'transl_except (pos:643. .645, aa:Xaa)
'transl_except (pos:135. .1137, aa:Xaa)
'transl_except (pos:2809. .2811, aa:Xaa)
'transl_except (pos:2809. .2811, aa:Xaa)
'transl_except (pos:3040. .3042, aa:Xaa)
'transl_except (pos:308. .3210, aa:Xaa)
'transl_except (pos:300m. aa:Xaa)
'transl_except (pos:300m. aa:Xaa)
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"C>T mutation"
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"C>T mutation"
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Kinney R, Trent DW;
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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated nonstructural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DEN)-2/1-VP1 fusion protein related to the invention. This fusion protein contains attenuated DEN-2 DN-23V backbone comperising a valine at the non-structural protein (NS3)-250 and the premembrane/membrane protein (PPM) and an envelope protein (E) from wildtype DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                               Flavivirus, Dengue virus, DEN, vaccine, infection, virucidal, avirulent, immunogenic, viral disease, pharmaceutical, chimeric, ss.
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "DEN-2/1-VP1 fusion protein"
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0; Mismatches
                                                          1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                           Dengue virus (DEN)-2/1-VP1 chimeric cDNA
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97. .10272
/*tag= a
                                                                                                                                                                         AAD14614 standard; cDNA; 10723 BP.
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                                                                                                                                                                                                                                                                      (first entry)
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinney RM, Kinney CYH,
                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                     Dengue virus; type I.
Dengue virus; type II.
Chimeric.
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P-PSDB; AAE07993.
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01-NOV-2001
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Matches
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AAD14614
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The invention relates to avirulent, immunogenic flavivirus chimeras comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses alicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses uch as dengue virus seroctypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4) are mesquito-borne flavivirus pathogens. The flavivirus genome contains 5' non-coding region followed by a capsid protein (C) encoding region, premembrane/membrane protein (prw) encoding region, an envelope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric flaviviruses that are avirulent and immunogenic, useful for vaccinating against a range of dengue viruses.
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protein (EP encoding region, followed by the region encoding non-
structural proteins (NSI-NS2A-NS2A-NS4A-NS4B-NS5) and finally a
non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                 Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; avirulent; immunogenic; viral disease; pharmaceutical; ss.
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                                   136 AATATGCTGAAACGCGAGAAACCGCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 252-268; 470pp; English.
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                                                                                                                                                                                                                                                                         Wild-type, virulent DEN-2 16681 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
97. .10272
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nes 28; Conserva
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P-PSDB; AAE07986.
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01-NOV-2001
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Matches
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Search completed: August 3, 2004, 18:46:03 Job time : 154.5 secs

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Sequence 1259, Ap
Sequence 4107, Ap
Sequence 1156, Ap
Sequence 11497, A
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3, Appli
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                                                            August 3, 2004, 18:28:49; Search time 37 Seconds (without alignments) 419.963 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-09-252-991A-11497
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US-08-484-004-52
US-08-811-566-5
US-09-034-756-5
US-08-075-233-11
US-09-328-352-1888
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US-08-915-152-2
PCT-US96-07627-1
PCT-US96-07627-2
US-08-325-4268-1
US-09-078-173A-11
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US-08-611-107-32
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Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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No.
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28 16.8 60.0 1746 4 US-09-489-013A-6977 Sequence 29 16.6 59.3 297 4 US-09-131-294A-522 Sequence 31 16.6 59.3 297 4 US-09-131-294A-522 Sequence 31 16.6 59.3 792 4 US-09-134-000C-295 Sequence 3 16.6 59.3 258 4 US-09-134-00C-295 Sequence 3 16.6 59.3 258 4 US-09-134-00C-295 Sequence 5 34 16.6 59.3 10091 3 US-09-058-166A-214 Sequence 5 36 16.4 58.6 1404 4 US-09-620-312D-710 Sequence 5 36 16.4 58.6 1404 4 US-09-620-312D-710 Sequence 7 36 16.4 58.6 1404 4 US-09-620-312D-710 Sequence 7 36 16.2 57.9 403	6977, Ap	522,	314,	295, Ap	361, Ap	214, Ap	34,	105,	710	6	158, App	450, Ap	450, Ap		450,	693, App	17, App	1, Appl
28 16.8 60.0 1746 4 10.0 1746 4 10.0 1746 4 10.0 1746 4 10.0 1746 4 10.0 1746 1746 1746 1746 1746 1746 1746 1746	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence
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28 16.8 50.0 30 16.6 59.3 31 16.6 59.3 33 16.6 59.3 34 16.6 59.3 36 16.4 58.6 37 16.4 58.6 39 16.2 57.9 41 16.2 57.9 45 16.2 57.9	4	4	4	4	4	4	m	4	4	4	4	4	4	4	4	m	4	٣
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ALIGNMENTS

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We sequence 1. Application US/08669423

Sequence 1. Application US/08669423

Patent No. 6455504

Determ No. 645550

CENERAL INFORMATION:
APPLICANT: RAVIPERABA, Kanakatte
APPLICANT: RAVIPERABA, Kanakatte
APPLICANT: RAVIPERABA, Kanakatte
APPLICANT: Hayes, Curtis G.
TITLE OF INVENTION: Neutralizing Antibodies
NUMBER OF SUNDENTION: Neutralizing Antibodies
NUMBER: Rebeeds
STREET: 8901 Wisconsin Ave., Bidg. 1, T-12
COMPUTER: Beheeds
SOFTWAR: PROPALICATION DATA:
COMPUTER: Plops of Sundentin Release #10, Version #1.30B
SOFTWAR: PREDICATION NUMBER: US 60/017,839
FILING DATE:
CLASSIFICATION NUMBER: US 60/017,839
FILING DATE:
APPLICATION NUMBER: U
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 2310
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LOCATION: 1218
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                                                                       PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
AUTHORS: Woo, WS.
AUTHORS: Woo, WS.
AUTHORS: Wright, P J
TILLE: Partial nucleotide sequence and deduced amino
TITLE: Authors type 2. New Guinea C and PUO-218 strains
JOURNAL: J. Gen. Virol.
VOLUME: 69
PAGES: 1998
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Patent No. 6138561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

100.0%; Score 28; DB 4; Length 2357;

Best Local Similarity 100.0%; Pred. No. 0.00085;

Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                PUBLICATION:
AUTHORS: Inie, K
AUTHORS: Mohan, P M
AUTHORS: Basaguri, Y
AUTHORS: Putnak, R
AUTHORS: Padmanabhan, R
TITLE: Sequence Analysis of Cloned dengue virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STRAIN: New Guinea C
SOSTITION IN GENOME:
CHROMOSOME/SEGMENT: Prem and Envelope
MAP POSITION: 330-2446
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Padmanabhan, R
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: Vakharia, V N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION: AUTHORS: Yaegashi, T
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Sasaguri, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006-1812
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197-211
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AUTHORS:
AUTHORS:
JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-869-423-1
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Patent No. 6136561

GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
NAWE/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Membrane"
                                                                                                         NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
FEATURE:
                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 2326
COTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
AUTHORS: Hahn, Y.S.
JUUNNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELEPHONE: (202) 887-0763
TELEFANGE: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AATATGCTGAAACGCGAGAAACCGCG 28
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Best Local Similarity 100.
Matches 28; Conservative
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US-08-937-195-2
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NAME/KAY: MISC_IEGALURE

COCATION: 1216.1218

OTHER INFORMATION: Anote= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PRISS
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: ditation= ([1])
FEATURE:
NAME/KEY: misc_feature
IOCATION: 1258.1260
OTHER INFORMATION: Anote= "GTG(coding for Val) is
OTHER INFORMATION: Anote= "GTG(coding for Val) for the wild-type DEN-2 PRISS
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: misc_feature
IOCATION: 1762..1764
OTHER INFORMATION: Anote= "ATT(coding for Ile) is
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: misc_feature
IOCATION: 1927..1929
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: misc_feature
IOCATION: 1927..1929
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: misc_feature
IOCATION: 1927..1929
OTHER INFORMATION: Anote= "AGT(Coding for Ser) is
OTHER INFORMATION: Actation= ([1])
FEATURE:
NEARINE INFORMATION: Anote= "AGT(coding for Ser) for the wild-type DEN-2 PRISS
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: misc_feature
IOCATION: 1927..1929
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Actation= ([1])
FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Actation= ([1])
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OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for Capsid"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Start of coding strand sequence of Membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: sequence of Membrane"
FEATURE:
SEATURE:
SEATURE:
SEATURE:
FEATURE:
                MOLECTUE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2(DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/81
FEATURE:
                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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AUTHORS: Hahn, Y.S.
JOURNAL: Virology
                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1..3381
linear
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DB 3; Length 3381;

100.0%; Score 28;

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Sequence 2, Application US/08915152
Patent No. 616547
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCE: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
O'THER INFORMATION: /note= "Start of coding strand
O'THER INFORMATION: sequence for Capsid."
                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1929—
OTHER INFORMATION: /note= "C is replaced by T for
OTHER INFORMATION: wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 2310 OTHER INFORMATION: /note= "A is replaced by N for OTHER INFORMATION: Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Start of coding strand
sequence for preMembrane"
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                                                                                                                                                       by A for
                                                                                     NAME/KEY: misc_feature
LOCATION: 1762_
OTHER INFORMATION: /note= "G is replaced
OTHER INFORWATION: Wild-Type sequence"
FEATURE:
OTHER INFORMATION: Wild-Type sequence" FEATURE:
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OTHER INFORMATION: /note= "Start of of OTHER INFORMATION: sequence for NSI" PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 343—
OCHER INFORMATION: /note= "Start of
OTHER INFORMATION: sequence for prew
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LOCATION: 2326
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Virology
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DATE: 1988
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STATE:
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LOCATION: group(103, 1940, 1991, 2025)
OTHER INFORMATION: /note="Positions in the SI strain
OTHER INFORMATION: representing corrections to the wild type DEN-2 PRI59 strain
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /citation= {[1]}
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                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08915152
Patent No. 6165477
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: DC
COUNTRY: DC
COUNTRY: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFERMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/915,152
FILING DATE: 20-AUG-1997
CLASSIFICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995
CLASSIFICATION NUMBER: 29,959
FILING DATE: 10-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MUTABALIGE, KATE H.
REGISTRATION NUMBER: 29,959
TELEPHONE: (202) 897-1500
TELEPHONE: (202) 897-1500
TELEPHONE: (202) 897-1503
TELEPHONE: (202) 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUDRESSEE: MORRISON & POERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
                             0.00091;
hes 0;
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                   Best Local Similarity 100.0%; Pred. No. 0.(
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                  40 AATATGCTGAAACGCGAGAGAAACCGCG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1218
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LOCATION: 1260
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CLONE: Den-2 PR159/S1
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US-08-915-152-1
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Gape

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representing corrections to the wild type DEN-2 PR159 strain reported by Hahn(Citation #1)" /citation= ([1])
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FCT-USSG-07627-1

FCT-USSG-07627-1

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BM PC compatible

COMPUTER: SEQUENCE: PC-DOS/MS-DOS

SOFTWARE: PATATION NUMBER: PCT/US96/07627

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3381 base pairs

TYPE: NUCLECIE ATPE: CONA

CORGANISM: Dengue virus

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CONA

CLONE: Den-2 PRI59/S1

FRATURE:

CLONE: Den-2 PRI59/S1

FRATURE:

MANA/VEV.
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100.0%; Pred. No. 0.00091;
tive 0; Mismatches 0; Indels
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LOCATION: group[103, 1940, 1991, 2025)
OTHER INFORMATION: /note= "Positions in the SI strain
OTHER INFORMATION: representing corrections to the will
OTHER INFORMATION: reported by Hahn(Citation #1)"
OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for preMembrane"
NAME/KEY:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence of Envelope"
FEATURE:
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LOCATION: 1218
LOCHER INFORMATION: /note= "G is replaced by A for
OTHER INFORMATION: wild-Type sequence"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
AUTHORS. Hahn, Y.S.
JOURNAL: Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Best Local Similarity 100.0
Matches 28; Conservative
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; DATE: 1988
US-08-915-152-2
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LOCATION: 1216_1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15
OTHER INFORMATION: scrain(citation #1)"
FEATURE INFORMATION: /citation= [[1]])
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LOCATION: 1258.1260
COTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced for GTT(coding for Val) for the wild-type DEN-2 PRIS
OTHER INFORMATION: Strain(Citation #1)"
COTHER INFORMATION: /citation= ([1])
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LOCATION: 1762_1.764
COTHEN INFORMATION: //note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
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OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
     COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-70L-1995
PTILING DATE: 10-70L-1995
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-70L-1995
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-70L-1995
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-70L-1995
APPLICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEFAM: (202) 887-1500
TELEFAM: (202) 887-1500
TELEFAM: (202) 887-150
TELEFAM: 10-430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYRANDEDNESS: single
TOPOLOGY: linear
OMCHECULE TYPE: CDNA
ORGANISM: Dengue virus
STRAIN: Serctype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: DEN-2 PRISS/SI
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LOCATION: 1927.1929
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343
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LOCATION: 1..3381
FEATURE:
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TITLE OF INVENTION: SUBUNIT VACCINE AGAINST FLAVIVIRUS INFECTION
NUMBER OF SEQUENCES: 50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1929
OTHER INFORMATION: /note= "C is replaced by T for
OTHER INFORMATION: Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1
LOTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid."
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sequence for preMembrane"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Envelope"
                                           /note= "T is replaced by G for
Wild-Type sequence"
                                                                                                                                                                                                                                                                                                                                                                                                /note= "A is replaced by N for
Wild-Type sequence"
                                                                                                                                  LOCATION: 1762
OTHER INFORMATION: /lote= "G is replaced by A OTHER INFORMATION: Wild-Type sequence"
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100.0%; Score 28; DB 5; L
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0;
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LOCATION: 343
OTHER INFORMATION: /note
OTHER INFORMATION: seque
FEATURE:
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 2310
OTHER INFORMATION: /not
OTHER INFORMATION: Wild
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LOCATION: 2326
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NAME/KEY: misc_feature
                                                                                                               NAME/KEY: misc_feature
                LOCATION: 1260
OTHER INFORMATION:
OTHER INFORMATION:
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, PAGES: 167-180
, DATE: 1988
PCT-US96-07627-1
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NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: Strain(Citation #1)"
OTHER INFORMATION: Strain(Citation #1)"
FOTHER INFORMATION: /citation= ([1])
FOTHER INFORMATION: /citation= ([1])
NAME/KEY: misc_feature
LOCATION: 1762..1764
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1.3381
FBATURA
NAME/KEY: misc feature
LOCATION: 1216_.1218
OTHER INFORMATION: replaced by GAA(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR15:
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
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COTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: /citation= ([1])
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OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(citation #1)"
OTHER INFORMATION: ditation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for Capsid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 343 _ OTHER INFORMATION: /note= "Start of coding strand OTHER INFORMATION: sequence for preMembrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 616—
LOTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
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OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
                 APPLICATION NUMBER: PCT/US96/07627
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGHH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                            ORGANISM: Dengue virus
STRAIN: Serotype 2(DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: stra
OTHER INFORMATION: /cit
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: 2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
CURRENT APPLICATION DATA
                                                                                                                                                                                                                  MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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65.7%; Score 18.4;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ropology: linear
                                                                                                                                                                                                                                                                                                    LENGTH: 1443
                                                                                                                                                                                                                                                                                                                                                           US-09-078-173A-11
                                                                                                                                                                                                                                                                               SEQ ID NO 11
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Pred. No. 0.0063;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FU, Jianlin
APPLICANT: FU, Jianlin
APPLICANT: TAN, Boon-Haun
APPLICANT: TAN, Yap.-Cheong
APPLICANT: CHAN, Yin-Hwee
TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
TITLE OF INVENTION: (SINGAPORE STRAIN)
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON and VANDERHYE PC
                                                                                                               Query Match
100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Rioppy disk

COMPUTER: In PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DAMPER: US/08/325,426B

INFORMATION FOR SEQ ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 10718 base pairs

TYPE: nucleic acid

STRANDEDMESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA sequence corresponding to

HYPOTHETICAL: NO

HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: NIXON and VANDERHYE PC
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SONGES:
ORGANISM: Dengue Fever Virus Type 1
STRAIN: $275/90
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                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08325426B Patent No. 6017535
GENERAL INFORMATION:
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Best Local Similarity 96.4%;
Matches 27; Conservative (
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LOCATION: 81..10268
VOLUME: 162
PAGES: 167-180
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                                                      , DATE: 19
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US-08-224-391-52
| Sequence 5.2, Application US/08224391
| Patent No. 5744140
| GENERAL INFORMATION:
| APPLICANT: Pacletti, Enzo
| TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
| TORRESPONDENCES: 93
| CORRESPONDENCES: 93
| CORRESPEE: Curtis, Morris & Safford
| ADDRESSEE: Curtis, Morris & Safford
| ADDRESSEE: Curtis, Morris & Safford
| STREET: 530 Fifth Avenue
| STREET: New York
| COUNTRY: United States of America
| IN ONE TO COMPANDE FORM: | MORE TO COMPANDE FORM: |
| COMPUTER: READABLE FORM: | MORPH TYPE: Floppy disk |
| COMPUTER: PatentIn Release #1.0, Version #1.25 |
| CURRENT APPLICATION NUMBER: US/08/224,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.7%; Score 18.4; DB 3; Length 1443; Best Local Similarity 78.6%; Pred. No. 21; Matches 22; Conservative 0; Mismatches 6; Indels 0
APPLICANT: Ian M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Alan Slusarenko
APPLICANT: Alan Slusarenko
APPLICANT: Alan Brash
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REPERENCE: 06027.0001
CURRENT APPLICATION NUMBER: US/09/078,173A
CURRENT APPLICATION NUMBER: US/09/078,173A
KUNBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2340
TELECHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               933 AAAATGCTGAGATGCAAGAGAAACTGAG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Capsicum annum (green pepper)
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TELEPAX: (212) 840-0712
INFORMATION FOR SEQ 1D NO: 52: SEQUENCE: CHARACTERLSTICS: LENGTH: 4512 base pairs
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DB 1; Length 4512;

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Length 12980;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
      ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                           COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eleopy disk
COMPUTER: Compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/811,566
FILING DATE: 03-MAR-1997
CLASSIFICATION NUMBER: 1997
CLASSIFICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1113-1-006
TELEFONE: 201-487-5800
TELEFONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LEMOTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 5, Application US/09034756
Patent No. 6392028
GENERAL INPORMATION:
GENERAL INPORMATION: CHARLES et al.
APPLICANT: RICE, CHARLES et al.
ITTLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.7%; Score 18.4; I 78.6%; Pred. No. 33; Live 0; Mismatches
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APPLICATION NUMBER: US/09/034,756
FILING DATE: 04-May-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9714 AATATGCTAAAACGCGGCATACCCCGCG 9687
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.6
Matches 22; Conservative
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                                                                                                    Hackensack
: New Jersey
RY: USA
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                                                                            Floor
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                                                                                                        CITY: Hac
STATE: Ne
COUNTRY:
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                                                                            STREET:
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                                         Gaps
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                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/08484304
| Patent No. 5744141
| GENERAL INFORMATION: PADOLETI, Enzo
| APPLICANT: Pincus, Steven E. | TILE OF INVENTION: PLAVIVIRUS RECOMBINANT POXVIRUS VACCINE NUMBER OF INVENTION: PAPALOS. 93
| CORRESPONDENCE ADDRESS: | Safford ADDRESSEE: Covitie, Morris & Safford ADDRESSEE: Covitie, Morris & Safford ADDRESSEE: Covitie, Morris & Safford ADDRESSEE: Covitie, New York STREET: New York STRIE: New York STRIE: New York STRIE: Now York 
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Patent No. 6127116
GENERAL INFORMATION:
APPLICANT: Rice, Charles et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
PILING DATE:
                                         . 9
Best Local Similarity 78.6%; Pred. No. 26; Matches 22; Conservative 0; Mismatches
                                                                                                        1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                                                                                                                                       43 AATATGCTGAAACGCGGCTTACCCCGCG 70
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REGISTRATION NUMBER: 25,506
REGISTRATION NUMBER: 454310-2340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPHONE: (212) 840-333
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/224,391
FILING DATE:
APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-JUL-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.6'
Matches 22; Conservative
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113 AGATGCTGAAACTCAATAGAACCCTCG 139
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Job time : 38 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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US-09-328-352-1888/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence 11, Application US/08875233

Sequence 11, Application US/08875233

Sequence 11, Application US/08875233

Patent No. 6127601

APPLICANT: Boeshore, Maury L

APPLICANT: Tricoli, David M

APPLICANT: Tricoli, David M

APPLICANT: Tricoli, David M

APPLICANT: Reynolds, John F

APPLICANT: Carney, Kim J

TITLE OF INVENTION: Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: 1111018

CUNNEX: 10.S.A.

ZIP: 60089

COMPUTER READBALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION NUMBILE:
NAME: Lisa v. Mucaller
TELEFHONE: 312-616-5460
TELEFAX: 312-616-5400
TELEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9714 AATATGCTAAAACGCGGCATACCCCCGCG 9687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                                                                   ; MOLECULE TYPE: CDNA
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-034-756-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: CUCUMBER MOSAIC VIRUS STRAIN: WHITE LEAF
                           TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..657
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2 Pruden
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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ANTI-SENSE: N
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Sequence 1888, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1888
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AUTHORS: Quemada, H
AUTHORS: Kearney, C
AUTHORS: Gonsalves, D
AUTHORS: Slightnom, J
TITLE: Owner, Slightnom, J
TITLE: Owner, Stains C
TITLE: Virus Strains C and WL RNA 3
JOURNAL: J. Gen. Virol.
VOLUME: 70
PAGES: 1065-1073
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IndelB
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                                                                                                                                                                                                                                                                                            62.1%; Score 17.4; D 77.8%; Pred. No. 56; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.1%; Score 17.4; D
Best Local Similarity 77.8%; Pred. No. 59;
Matches 21; Conservative 0; Mismatches
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Sequence 2, Appli
Sequence 23, Appl
Sequence 23, Appl
Sequence 3252, A
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Sequence 11, Appl
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                                                                                                                                                             3, 2004, 18:40:54; Search time 158 Seconds (without alignments) 868.911 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBF PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBF PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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100.0 3381 15 US-10-247-960-2

92.9 26 9 US-09-840-707A-23

67.1 1428 16 US-10-038-857A-23

66.4 1602 15 US-10-156-761-2266

66.4 9025608 15 US-10-156-761-1

65.7 12980 9 US-09-238-076-5

65.7 12980 10 US-09-938-937-5

65.7 12980 10 US-09-938-956-95

65.7 12980 10 US-09-938-956-97

65.0 452 10 US-09-918-958-7460

65.0 2179 13 US-09-821-245A-434

65.0 9875 10 US-09-764-891-7878
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                                                                                                                                                                                                                                                                                                                                          1 aatatgctgaaacgcgagagaaaccgcg 28
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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28
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Sequence 130933, Sequence 11819, A Sequence 3468, Ap Sequence 2508, Ap Sequence 2571, Ap Sequence 553, App	29374 9, App 9, App 9, Ap 20, A	23394 23394 33394 22, 237	equence 21920, equence 3, p equence 5, p equence 2, p equence 1, p equence 1, p equence 13, p equence 1990
10-424-599-130933 10-198-846-11819 10-198-846-3468 10-398-221-2508 10-398-221-2571 10-398-221-553	5282-1228-29374 S 319-9948-1 5-398-221-9 5-398-221-9 5-398-221-2058 5-398-321-3058 5-398-321-3058 5-398-31-3058 5-398-31-3058	0-437-963-17200 0-424-99-53946 0-424-532-237136 0-027-632-237136 0-282-122A-39862 0-282-122A-39862 0-011-033-11 9-738-269-22 0-011-033-11 9-738-269-22	10-171 103 - 23 10-371 - 101 - 3 10-371 - 101 - 5 10-371 - 101 - 5 10-309 - 933 - 1 10-322 - 281 - 33 10-087 - 192 - 1990
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ALIGNMENTS

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Gaps
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                   Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
APPLICANT: WORN, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
CURRENT FILING DATE: 2002-06-18
; PRIOR PILING DATE: 2001-03-01
; NUMBER: OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-247-960-2
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; RENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Primer US-10-085-944-2
US-10-085-944-2
                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Sequence 5, Appli Sequence 5, Appli Sequence 27460, A Seguence 434, App Seguence 7878, Ap

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RESULT 5
US-10-369-493-32952/c
US-10-369-493-32952, Application US/10369493
; Sequence 32952, Application US/10369493
; Sequence 32952, Application US/10369493
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
; APPLICANT: APPLICANT: Slater, Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE REFERENCE: 39-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fredeking, Terry M.
APPLICANT: Fredeking, Terry M.
APPLICANT: George M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
TITLE OF INVENTION: INTECTIONS AND OTHER DISORDERS
TITLE OF INVENTION: LONG DATE: 2002-06-05
CURRENT APPLICATION NUMBER: US/10/038,557A
CURRENT APPLICATION NUMBER: 09/840,707
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Artificial Sequence
FRATURE:
CHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
CHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred, No. 1.5e+02;
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 32952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 CGGAACCGCGAGAGAACCGCG 1163
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US-10-156-761-2266
S. Sequence 2266, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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Best Local Similarity 90.9%;
Matches 20; Conservative
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; ORGANISM: Xylella fastidiosa
US-10-369-493-32952
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US-09-840-707A-23
US-09-840-707A-23

Sequence 23, Application US/09840707A

Sequence 23, Application US/09840707A

Sequence 23, Application US/09840707A

Patent No. US20020077276A1

GENERAL INFORMATION:

APPLICANT: Fredeking, Terry M.

APPLICANT: Ignatyev, George M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS

TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS

FILE REFERENCE: 24881-301C

CURRENT APPLICATION NUMBER: US/09/840,707A

CURRENT FILING DATE: 2001-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 23

LEAST SECTION NUMBER OF SEQ ID NOS: 26

LEAST SECTION NOT SETION NUMBER OF SEQ ID NOS: 26

SEQ ID NO 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0
APPLICANT: Peters, lain
APPLICANT: Coller, Beth-Ann
APPLICANT: Coller, Beth-Ann
APPLICANT: McDonell, Michael
APPLICANT: McDonell, Michael
APPLICANT: Harada, Kent
TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
TITLE OF INVENTION: AGAINST FLAVIVIRAL INPECTION
FILE REPERENCE: 24733-20005.01
CURRENT PILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 08/376,463
PRIOR PELING DATE: 1999-08-18
PRIOR PELING DATE: 1999-08-18
PRIOR PELING DATE: 1999-08-18
PRIOR PELING DATE: 1999-08-18
SPRIOR PELING DATE: 1999-08-18
SEQ ID NOS: 37
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 92.9%; Score 26; DB 9; Length 26; Best Local Similarity 100.0%; Pred. No. 0.046; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AATATGCTGAAACGCGAGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 AATATGCTGAAACGCGAGAGAAACCGCG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-10-038-557A-23
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Sequence 23, Application US/10038557A

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Query Match 65.7%; Score 18.4; DB 14; Length 1443; Best Local Similarity 78.6%; Pred. No. 2.2e+02; Matches 22; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                       APPLICANT: Inn M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Duncan Gaskin
APPLICANT: Duncan Gaskin
APPLICANT: Duncan Gaskin
APPLICANT: Nathalie Tijet
ITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
ITLE OF INVENTION: LYALE AND USES THERBOF
ITLE REFERENCE: 06027.0001U3
CURRENT PAPLICATION NUMBER: US/10/042,991
CURRENT PILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09238076
Sequence 5, Application US/09238076
Patent No. US20020102540A1
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/238,076
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933 AAAATGCTGAGATGCAAGAGAAACTGAG 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Capsicum annum (green pepper)
US-10-042-991-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/034,756
                                      Sequence 11, Application US/10042991
Publication No. US20020142407A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION UNMBER: 35,197
REFERENCE/DOCKET UNMBER: 6029-
TELECOMMUNICATION INFORMATION:
TELEFAK: 314,727-5188
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12980 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MO
COUNTRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic
STRANDEDNESS:
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          US-10-042-991-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; DB 15;
1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 66.4%; Score 18.6; DB 15;
1 Similarity 84.0%; Pred. No. 3.7e+02;
21; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

: LOCATION: (4187715)

: OTHER INFORMATION: a, t, c, g, other or unknown

US-10-156-761-1
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84.0%; Pred. No. 1.8e+:
cive 0; Mismatches
APPLICANT: ISHLKAWA, UNN
APPLICANT: ISHLKAWA, HIROSHI
APPLICANT: SHIRAW, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26.
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
SRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2266
LENGTH: 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION;
JOHNSTAN INFORMATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.09
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1602)
US-10-156-761-2266
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Best Local Similarity
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Gaps

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Sequence 5, Application US/09917563
Publication No. US20030073080A1
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
APPLICANT: RICE, CHARLES et Al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
VIRUS (HCV) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-917-563-5
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                                                                                                                                              Query Match 65.7%; Score 18.4; DB 9; Length 12980; Best Local Similarity 78.6%; Pred. No. 3e+02; Matches 22; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    UDIICATION NO.
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
VIRUS (HCV) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPER FOCOMPATIBLE
COMPUTER: IADAPP disk
COMPUTER: IADAPP COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/995,937
FILING DATE: 28-No. US20030028010A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/034,756
FILING DATE: 04-May-1998
ATTORNEY AGENT INFORMATION:
NAME: HOLLAND: DONALD R.
REGISTATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
TELEFRAN: 314-727-5188
TELEFRAX: 314-727-5092
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                  9714 AATATGCTAAAACGCGGCATACCCCGCG 9687
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US-09-995-937-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09995937
Publication No. US20030028010A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                       MOLECULE TYPE: CDNA HYPOTHETICAL: NO
  linear
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                                                                      ; ANTI-SENSE: NO
US-09-238-076-5
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-995-937-5/c
TOPOLOGY:
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RESULT 11 US-09-917-563-5/c

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Pred. No. 3e+02;
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                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREFACTION RELEASE #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,563
FILING DATE: 27-Jul-2001
CLASSIFICATION NUMBER: 09/238,076
FILING DATE: 26-JAN-1999
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REFERENCE/DOCKET NUMBER: 35,197
RESTRANDON INFORMATION:
TELEPHONE: 314-727-5188
TELEPHONE: 314-727-6092
INFORMATION FOR SECID NO: 5:
SEQUENCE CHARACTERISTICS:
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; Sequence 27460, Application US/09918995
; Publication No. US20030073623A1
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REPERBNCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 1999-01-20
; RICA APPLICATION NUMBER: US/09/235,076
; RICA REPERBORE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PeatsEQ for Windows Version 3.0
; SEQ ID NO 27460
; LENGTH: 452
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NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.6%;
Matches 22; Conservative
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                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                      STATE: MO
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Score 18.2; DB 10; Length 9875; Pred. No. 3.6e+02;
65.0%;
87.0%;
Query Match
Best Local Similarity
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APPLICANT: Agostino, Michael J.
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6401
FILE REFERENCE: 2001-03-29
FILE REPLACATION NUMBER: 60/194,941
FRIOR APPLICATION NUMBER: 60/194,941
FRIOR APPLICATION NUMBER: 60/194,941
FRIOR PLING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 434
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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; Squence 7878, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SEQ ID NO 7878
; LENGTH: 9875
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                                                                                                              Query Match 65.0%; Score 18.2; DB 10; Length 452; Best Local Similarity 87.0%; Pred. No. 2.3e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1550 AAGATGCTGAAACAGGAGAAA 1572
                                                                                                                                                                                                                                                        172 AAGATGCTGAAACAGGAGAGAAA 194
                                                                                                                                                                                                              1 AATATGCTGAAACGCGAGAAA 23
                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 434, Application US/09823245A; Publication No. US20020039760A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AATATGCTGAAACGCGAGAAA 23
NAME/KEY: misc_feature
| LOCATION: (1)...(452)
| OTHER INFORMATION: n = A,T,C or G.
US-09-918-995-27460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.0*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-891-7878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-823-245A-434
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US-09-764-891-7878/c
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Sequence 130933, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J

APPLICANT: APPLICANT: AND YIMUA

APPLICANT: APPLICANT: Chou YiMua

APPLICANT: Chou YiMua

APPLICANT: Chou YiMua

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

EBNGTH: 529
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  3; Indels
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83.3%; Pred. No. 4.4e+02;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT3847_8923C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(529)
OTHER INFORMATION: unsure at all n locations
0; Mismatches
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Job time : 171 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 ATGAAGCAACGCGAGGGAAACCGC 158
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                                                                  1 AATATGCTGAAACGCGAGAAA 23
20; Conservative
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Matches 20, Conservative
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                                                                                                                                                                     US-10-424-599-130933
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  Matches
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us-10-085-944-2.rst

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyprinidae; Danio.

I (bases 1 to 776)
S NIH-MGC http://mgc.nci.nh.gov/.
S NIH-MGC http://mgc.nci.nh.gov/.
L Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: Gappa-rémail.nh.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G. Consortium (LLNL)
DNA Sequencing by: Agencutt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
           CF512236 CAbud0003
BE841207 QV4-SN002
BAL487728 T. ANO92
AL464374 T. brucei
BE776235 MY-12-F-0
AL647635 MY-12-F-0
AL647635 MY-12-F-0
AL64763 AL647632
CCA349616 629008 NC
CCA349616 629008 NC
CCA349616 62908 NC
CCA349616 CA340
CCA349616 CA340
CCA3436 TESTOLG T
BCG59281 NCBTQ8b5
CCP939381 NCBTQ8b5
CCP939381 NCBTQ8b5
CCP939381 NCBTQ8b5
CCP939381 NCBTQ8b5
AL014632 F. rubripe
AL014632 F. rubripe
AL014632 F. rubripe
AL014632 F. rubripe
ANO724090 HS. STAFA
BZ130571 CH210-394
CB0200289 PX67F07-Y
BZ130571 CH210-394
CB0200289 PX67F07-Y
BZ13278 SCEPLB104
BH59312 BOHBP93TR
CX126303 HA MX23
BE615972 601279483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCOURT 16394292 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7037741 5', mRNA Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ132164 CH230-394
BF678988 602153627
BI753870 603027558
BF620613 HVSMEC002
AL077950 Drosophil
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BF690226 602186576
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                                                                   AQ945692
BTA140D12P
BTA16215
AL647619
AL647619
AL647619
CA356841
CA356841
CA356841
CA356841
CA356841
CA356841
CP995511
CP995511
BG659286
CF19855
CF198531
BG659281
AQ657703
FR0021761
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CG016439
AW599270
AW599270
CB020289
BR130571
CB020289
BH929269
BH929269
BH9592069
BH55870
BR615972
BR6
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Danio rerio
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697
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CF996467/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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CF455745 AGENCOURT
CB078143 hj63h04.g
CF372439 CSECS052D
                                                                                                                     August 3, 2004, 18:26:44; Search time 1253 Seconds (without alignments) 667.311 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                 55026578
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        1 aatatgctgaaacgcgagagaaaccgcg 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF996467
CF455745
CB078143
CF372439
                                                                                      - nucleic search, using sw model
                                                                                                                                                                                                                                                                       IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em gss mus: em gss pro: em gss rod: em gss phg: em gss vrl: gb gssl: *
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seq length: 200000000
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gb_est5:*
em_estfun:*
em_estfun:*
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em_estin:
em_estwu:
em_estov:
em_estpl:
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em_htc:*
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28
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gb_htc: *
gb_est3: *
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301
712
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em_gas_f
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70.7
70.0
70.0
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Score

Result Š. 20.6 19.8 19.6 19.6

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/organism="Hedyotis terminalis"
/mol type="mRNA"
/db _tref="taxon:219667"
/db _tref="taxon:219667"
/dl _tref="taxon:219667"
/dlone="hj63h04"
/dev stage="pre-anthesis; Stage 2"
/dlone=hj63h04"
/dev stage="pre-anthesis; Stage 2"
/dlone=lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/dlone=lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/dlone="crogan: flower; Vector: pBK-CMV; Site 1: XhOI;
Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
SHL_12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: Not1; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb. Library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB078143 301 bp mRNA linear EST 24-JAN-2003 hj63h04.gl Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis terminalis cDNA clone hj63h04, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hedyotis terminalis
Hedyotis terminalis
Hedyotis terminalis
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Gentlanales; Rubiaceae; Rubioideae;
Spermacoceae; Hedyotis.
1 (bases I to 301)
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                    Length 720;
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Contact: W. Richard McCombie
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tal: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                    Score 19.8; DB 14;
Pred. No. 3.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mccombie@cshl.org
Plate: hj63 row: h column: 04
Seg primer: -21M13UnivRev
High quality sequence stop: 301.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 rargcrgaaacgrgacagaagcggcg 237
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CB078143.1 GI:27891580
                                                                                                                                                   Invitrogen."
                                                                                                                                                                                                                                                ch 70.7%;
1 Similarity 91.3%;
21; Conservative
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Best Local Similarity
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Best Local (
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CB078143
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                                                                                                                                                                                                                                  /moi type="mrkha"
//db xref="taxon:7955"
//clone="INARA"
//tissue type="whole body"
//lab_host="Mhines"
//lab_host="Dhines"
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Unpublished (1999)
Office of Cancer Genomics
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAo7 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.lnl.gov
Plate: NDAMS81 row: k column: 02
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 720)
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AGENCOURT_15376947 Human Anterior Horn Homo sapiens cDNA clone IMAGE:30515857 5', mRNA sequence.
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/tlssue_type="Peripheral Nervous system"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="Human Anterior Horn"
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLhM1478B row: e column: 03
High quality sequence stop: 734.
Location/Qualifiers
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High quality sequence stop: 544.
Location/Qualifiers

1. 720
/ organism="Homo sapiens"
/ mol type="mRNA"
/ db_xref="taxon:9606"
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Best Local Similarity 85.2%;
Matches 23; Conservative (
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CF455745
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/clone lib="Cabbau Normalised Flower Stage 12 (FLON0012)"
/note="Corpan: Inflorescence including flowers, Vector:
pZL; Normalised CDNA library from immature inflorescences
at stage 12 of the modified B-L system. Tissue collected
from field grown plants. A description of the modified B-L
system can be found in the paper by B. G. Combe' Adoption
of a system for identifying grapevine growth stages'
(1995) Aust. J. Grape and Wine Res. 1: 104-110."
                  CF372439 T12 bp mRNA linear EST 27-AUG-2003
CSECS052D08 FLOn0012 CabSau Normalised Flower Stage 12 (FLOn0012)
Vitis vinifera cDNA clone CSECS052D08 3', mRNA sequence.
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                                                                                                                                                Vitis vinifera
Vitis vinifera
Bukariota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermartophyta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermartophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
I (basea I to 712)
I (basea I to 712)
Iocco, P., Hua, C., Davies, C. and Thomas, M.R.
Expressed sequence tags from the grapevine cultivar Cabernet
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Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, Vitaceae, Vitis.
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berries at various developmental stages
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CAbud0003_IF_A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
Bud - CABUD Vitis vinifera cDNA clone CAbud0003_IF_A10 5', mRNA
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Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CCCAGTCACGACGTTGTAAAACG (M13 Forward)
                                                                                                                                                                                                                                                                                                                                                                                                                   CSIRO
PO Box 350, Glen Osmond, SA, 5064, Australia
Tel: 61 8 83038600
Email: Mark.R.Thomas@csiro.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"

culfivar="cabernet Sauvignon"

/db_xref="taxon:29760"

clone="CSECS052D08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Vitis vinifera"
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CF512147.1 GI:34543915
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Contact: Mark R. Thomas
CSIRO Plant Industry
                                                                                                         CF372439.1 GI:34319685
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Best Local Similarity 84.64
East Local 2; Conservative
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CF512147/C
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Anotes Organ: Bud; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CABUD is a cDNA library of Vitis vinifera cv. Cabernet sauvignon. Clone B dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. CDNAs were made by oligo-dT priming and directionally cloned. 5 and 3 adaptors were used in coloning as follows:
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1 (bases 1 to 734)
                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Pre-bloom (10-11 days before bloom)"
/lab_host="DHFslpha"
/clone lib="Vitis vinifera cv. cabernet sauvignon (Clone
8) Bud - CABUD"
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CAbud0003 IR A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
Bud - CABUD Vitis vinifera cDNA clone CAbud0003_IR_A10 3', mRNA
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Unpublished (200)
Contact: Douglas Cook, PhD
CAES Genome Facility
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Emai: 310 754 6561
Emai: GCCAAACGAATGGTCTAG.
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5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Library v
constructed using the Clontech Creator SMART and
fige-selected to contain the 0.5-3 kb size fraction.
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                                                                                                                                                                                                                                                                         /organism="vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon (Clone 8)"
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Contract: Douglas Cook, PhD
CABS Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGGACATATGCC.
                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:29760"
/clone="CAbud0003 IF_A10"
/sex="Hermaphrodite"
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Best Local Similarity 84.67
Erham 22; Conservative
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us-10-085-944-2.rst

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/Mol Lype="mins" or provided by the control of the 
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypansona bruce; (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
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project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBIO ISA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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T. brucei sheared genomic DNA clone 262h01, reverse sequence,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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ilarity 95.2%; Pred. No. 4.9e+02;
Conservative 0; Mismatches 1;
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                                                                                                               /organism="Homo sapiens"
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/strain="TREU927"
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   ity sequence stop: 248.
Location/Qualifiers
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/clone="262h01"
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1 (Bases I to 464)
1 (Barcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O', Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Bud; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CABUD is a cDNA library of Vitis vinifera cv. Cabernet Sauvignon. Clone B dissected bude. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&tc2=QV4-SN0024-200 Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE841207 200700-304-a07 SN0024 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                          /clone lib="Vitis" vinifera cv. cabernet sauvignon (Clone 8) Bud-- CABUD"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloning as follows:
5'-AAGCAGTGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART sit and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                       /mol_type="mRNA"
/cultivar="cabernet Sauvignon (Clone 8)"
/cultivar="cabernet Sauvignon (Clone 8)"
/cultivar="cabernet Sauvignon (Clone 8)"
/clone="cAbud0003_IR_A10"
/clone="CAbud0003_IR_A10"
/cex="Hermaphrodite"
/dev_stage="Pre-bloom" (10-11 days before bloom)"
/lab_nost="DHSalpha"
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                         'organism="Vitis vinifera"
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RESULT 9 AQ945692/c DEFINITION

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ORGANISM

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REFERENCE AUTHORS

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organism="Phytophthora infestans"
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Pred. No. 7.9e+02;
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/mol_type="genomic DNA"
/strain="TREU927"
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/clone="140d12"
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Wageningen University
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(bases 1 to 576)
                                                           Trypanosoma brucei
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E1-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
L. Unpublished (1999)
Other_GSSs: Sheared DNA-49GS.TR
Contact: Najib M. E1-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Gail and Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tdbd/
Class: shocgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Trypanosoma brucei"
/mol type="genomic DNA"
/strain="TREU927/4 GuTat 10.1"
/bb xref="taxon:5691"
/clone="Sheared DNA-49G5"
/clone="sheared DNA-49G5"
/clone="sheared DNA-49G5"
/clone="sheared DNA-49G5"
/clone="sheared DNA-49G5"
/note="Vector: DUCIB: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                         GSS 27-JAN-2000
                                                                                                                                                    AQ945692 568 bp DNA linear GSS 27-JAN-20
Sheared DNA-49G5.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-49G5, genomic survey sequence.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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67.9%; Score 19; DB 28; Length 568;
Best Local Similarity 81.5%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 5; Indels
       2 ATATGCTGAAACGCGAGAAACCGCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                  AQ945692.1 GI:6768880
                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 568)
                                                                                                                                                                                                                                                                                              Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                      rypanosoma.
                                                                                                                                                                                                                         AQ945692
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FEATURES

RESULT 10 TA140D12P LOCUS DEFINITION

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ACCESSION

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1. (Dagget, J.), Atkin, R.,

Rall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,

Ralville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Nelville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Norject, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TRED927/4 GUTet 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell. Oxford University Press, 1999).
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MY-12-F-04 PinfestansMY Phytophthora infestans cDNA, mRNA seguence.
BE776235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands 12 13 17 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 580)
Kamoun, S., Hraber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F.
Initial assessment of gene diversity for the comycete pathogen
Phytophthora infeatus based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Gape

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Query Match

DRIGIN

Best Loc Matches

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Ampliants accordingly memoral reporters reporters reproduced reporters remopodinae; Silurana.

I (bases 1 to 629)

Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (11_2003)

Unpublished (2003)

On Dec 13, 2001 this sequence version replaced gi:17655942.

Contact: Huckle E
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

constructed by Saron Surger Sanger Sange
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| Organism="Silurana tropicalis"
| /mol_type="mRNA"
| /db xref="taxmn:8364"
| /clone="TGas037f09"
| /dev stage="gastrula (stages 10.5-12 mixed)"
| /dab lib="XGC-gastrula"
| /done lib="XGC-gastrula"
| /done lib="XGC-gastrula"
| /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from sug of poly A+ RNA from stages 10-13 gastrulae. EcoRI which cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                              AL647632 ALC-gastrula Silurana tropicalis cDNA clone TGas037£09 5', mRNA sequence.
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CA349616
EST.
Oncorhynchus mykiss (rainbow trout)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota tropicas, Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Pred. No. 8.1e+02;
0; Mismatches 5; Indels
Indele
5.
Mismatches
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                                                                                                                                                                     202 araagcreaaagcceagagaaaacere 228
                                                                                       28
                                                                                       2 ATATGCTGAAACGCGAGAGAAACCGCG
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1 Similarity 81.5%;
22; Conservative (
22; Conservative
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Best Local Similarity
Matches 22; Conserv
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ORGANISM
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TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
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CA349616
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AL647632
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KEYWORDS
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                           /strain="DDR7562, Al mating type"
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/dev stage="taxon:4787"
/dev stage="taxon:4787"
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/dev stage="taxon:4787"
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/lab_host="E. coli, strain DH5-alpha"
/lab_host="PerfestansWr"
/loce="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
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S Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)

L Unpublished (2003)

On Mar 18, 2002 this sequence version replaced gi:19529975.

Contact: Taylor R

Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
CONSTRUCTED by Armon M. Zenopus Gene Collection (XGC) library
CONSTRUCTED by Armon M. Zenopus Gene Collection (XGC) library
CONSTRUCTED by Armon M. Zenopus Gene Collection (XGC) library
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CONSTRUCTED by Armon M. Zenopus Gene Collection (XGC) library
CONSTRUCTED by Armon M. Zenopus Gene Collect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCSIO7; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from sug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligsted into pCSIO7 with EcoRI at the 5' end and NotI at the 3' end."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%; Score 19; DB 10; Length 580;
ilarity 81.5%; Pred. No. 7.9e+02;
Conservative 0; Mismatches 5; Indels
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/lab_host="Escherichia coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TNeu062m06.plcSP6
Sequencing primer: SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silurana tropicalis (western clawed frog)
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/mol_type="mRNA"
/db_xref="taxon:8364"
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81.5%; Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 ATGAGCTGATACGCGAGAAGAACCGCG 351
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Location/Qualifiers
1. .602
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Oncorhynchus mykiss
but ayota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 633)

Servaca(C.E. and Keele,J.W.
Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002).
                                                                                                                                                                                                     Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876. Lectown Road, Kearneysville, WV 25430, USA
11876. Lectown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8140 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGGAPARATTCACACAGGA.
Location/Qualifiers
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Rexroad, C.E. and Keele, J.W.
Sequence analysis of a rainbow trout normalized cDNA library (npubblished (2002))
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/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Libzary made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oncorhynchus mykiss"
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Oncorhynchus mykiss
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/inte="Vector: pCMV Sport6; Site 1: Not1; Site 2: Sal1;
spleen, muscle from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
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